

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LENPHDSNLSGLFPLIDLDFSP*VLS CWASHTMENCS*LRSKRQITLWCS RMAE\LVYCLSWKCSHLKRHDFPM GKYQTPTCIDKGNMLYLSKLLGIES QCLGAEMGIPIKAMQSFTTSGRPKN EHSRNFVIIWKVLI
899	6396	A	930	1030	1384	LIALRKMGRNAQAQICIITSDG*NPS PLKTESTLKT\TQFSLYPWGEKFERT PSLMGQKNFR\TVCSQMSQMGAIQFQ/ HIQEWDERKSTITKKN*KDGEISW LECVMMNN\VTCTPDSMKK
900	6397	A	931	1	225	
901	6398	A	932	2	167	
902	6399	A	933	1	3339	PASVHPSVRPTVQRKGLQAGRTSTR GTEARRGAKSAADPCGPGQGTVA AMQSCARAWGLRLGRGVGGGRRL AGGSGPCWAPRSRDSSSGGDSAA AGASRLLERLLPRHDDFARRHIGPG DKDQREMLQTLGLASIDELIEKTVP ANIRLKRPLKMEDPVCENEILATLH AISSKNQIWRSYIGMGYYNCSVPQT ILRNLLENSGWITQYTPYQPEVSQ RLESLLNYQTMVCDITGLDMANAS LLDEGTAAAEALQLCYRHNKRKF LVDPR\CHPQTIAVVQTRAKYTGVL TELKLPCEMDFSKDVSGVLFQYP DTEGKVEDFTEL\VERAHQSGSLAC CATDLLALCILRPPGEFGVDIALGSS QRFQVPLGYGGPHAAFFAVRESLV RMMPGRMVGVTRDATGK\EVY\RL AP*KPREQHRRDKATSNICTAQAL LANMAA\MFAYHGSGLGHIA\RL RVHNATLILSEGLKRAGHQLQHDLF FDTLKIQCSCSVKEVLGAAQRQIN FRLFEDGTLGISLDET\NEKDLDDL LWIFGCESSAELVAESMGEECRGIP GSVFKRTSPFLTHQVFNSYHSETNIV RYMCKLENKDISLVHSMPLGSCTM KLNSSSELAPITWKEFANIHPFVPLD QAQGYQQLFRELEKDLCELTGHDQ VCFQPN\SGAQGEYAGLATIRAYLN QKGEHRTVCLIPKSAHG\TNPASAH MAGMKIQPVEVDKYGNIDAVHLK AMVDKHKENLAAIMITYPSTNGVF EENISDVCDLIHQHGGQVYLDGAN MNAQVGICRPGDFGSDVSHLNLHK TFCIPHGGGGPGMGPIGVKKHLAPF LPNHPVISLKRNEACPVGTVSAAP WGSSSILPISWAYIKMMGGKGLKQ ATETAILNANYMAKRL\ETHYRILFR GARGYVGHEFILDTRPFKKSANIEA VDVAKRLQDYGFHAPTMSWPVAG TLMVEPTES\EDKAELDRFCDAMISI RQEIADIEEGRIDP\RVNPLKNVLH TPLTCVTSSHWD\RPYSREVA\AFPLP FVKPENKFWPTIA\RIDDYGDQHL\A VCTCPPM\EVYESPF\SEQKRAVFLV LCSLSFKGIDFDGLSPEAFDKQERFH

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						LPTPSLK
903	6400	A	934	2	287	
904	6401	A	935	36	427	
905	6402	A	936	247	1183	CCWESPVDPQPLRQISGIALFCSFKE PPLLGLVHPNTKLRQGRKGCLKIN LLGPES\MAHIGGCDVYWGQQMGR VVKLENG*NRRPLPGFGSGPLAKPE DDEPCVWGDPLGIRGRGPKWGLLF VGR LHTRGLF*R*NPWETVKVKLLL SSETPI*GGRNMSF\VN DLTVTPGW KEDLISP NPKQQNGQRRKLPAFWV MGGHKMTGR LLEV*YCDPGK*KFY WTQLRFPNGVQPV S*KQTL SLVAET S\MARIRRVYVSGPDERR\ADLFVEN MPGFDPNIRPSSSGGYWVGMSTIRP *P\GSSMLD FL SERPWD
906	6403	A	937	179	516	VFSVLRAEDKICELLFCLKIKLFSAS FLVFRNQLPRKND FYSYEPSENPP ETGESVCLQLKSGAHL CRVCGCLG PKTCSRCHKAYYCSKEHQ TLDWRL GHKQACAQPGG
907	6404	A	938	41	274	KRGTERKTHFGGCSIQFS DIASGKNI LPGLCFLTHKR\WFC SL*RQGWVSR WSHE*GCTRCWRLGKFLWVADRFL GSG
908	6405	A	939	3	1111	CAPRQPAPRMAAAGARPVELGFAE SAPAWRLRSE\QFPSKVGG RPAWLG AAGLPGPQALACELCGRPLS FLLQV YAPL\PGR\PD A\FH\RCIFL FCCREQP \CCAGLARFLGIRLPRKND FYSYEP PSENPPPETGESVCLQLKSGAHL CR VCG\C*GPKTCSRCHKAILLAAREH QTL\DW EIGDIRQ\ACA QPDHL\DH I NFQDHNFPFFQEF EIVETEDEIMP* GVWKKEDYSRDY*GALG*STLKGR TWISM\AKHE\SRED\KFFQKF*NFRL ALGTEQDS*YAGRG\I APIWISGENIP QEKDIPDCPCGAKKILEFQVMPQLL NYLKADRLGKSIDWGILAAFTCAES CSLGTGYTEEFVWKQDVTDTP
909	6406	A	941	3458	4042	AGMIRRPSPWPSIRPPPAVFTNSCTS LQEPSGGTGRVQVPSIYQAS\STQIC VKGPD*GRNGKGNLSFGKAGIFHFP WCPKCPRPSSSPISMGLLSPEVDSVE R\PTFRFPLAPIYKECV*NGAG/AQ APDPRQKRGWPCHWNLMGVGRMP RVSPHLPEAWGPKHPDDRYTKGTA ICPRNHLPCDPRISAIGQPQG
910	6407	A	942	226	401	TSGDHWNI AVAPHENS DLLL VQGH DYKYRYFGLIVCVL*QAIVTPEEPQS IVPRLRTR
911	6408	C	943	211	282	MFYPPFNPRYFSVGFIAMNRHTD*
912	6409	A	944	1390	1698	HLFPHIKAGR*YGRPCREGILQ*KE* ETTGRHTCVLQGLAFQEVVVQVRN VFLHEALQLVKFAMQIFEVLLEKFP EPIVKHDL DQNT ECLFFRHMEKEHS SKK

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913	6410	A	945	27	412	IAEGNWCVYMPDIIWVFPPQAEAEEDCHSDTVRADDDEENESPA\ETDLQAQLQMF\RAQWMFELAPGVSSSNLENRPCRAARGSL\QKTSADTKGKQEQAKEEKLIIIDIVTNYIFFFWHMEIFTGHSK
914	6411	A	946	24	1489	GGSSAAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRSGPLPREDGCRTPGPQLLPLHGA\LLRPR TLLSSAAEDKARSRH\PD TQHPSSG GRCKGGTESPSSAAGRPASMAEAE\EDCHSDTVRADDDEENESPAETDV QALIP\MIQAQWKLEPAPRVSSSNLENRPCRAARGSLQKTSADTKGKQEQAKEEKARELFLQAVEEEQNGALYEAIKFYRRAMQLVPD\EFKITF\TRSPDGDGVGNSYIEDNDDSKMADLLSYFQQQLTFQESVLKLCQ\PELESSQIHISVLPMEVLMYIFRWVGSSDLDLTSL\EQLSLVCQRIPNLCPETPENMPVLALL*KFWGR\SC\IKLVSVTSPGRE DVF*ERPVR\VRFDGVYISKTTYIRQGEQSLDGFYRA\WH\QVEYYRYIRFFPDGHVMMMLTTPEEPQSIVPRLR\TREYQGLDAIPTGV TIRLSPRHRTIRTQSIWLLITKEKRKEKPL
915	6412	A	947	17	499	DRVLLCN\PRLECNGMITAHCSKP KPGSK*SSCFSLPSSWDY\KHEPPYRANLKNFFVETGSLYVAQAGFELLDSSNPPCFSLPKCWDYRPP*ATTPS\FKND SHFNFLNRF\SHFVVFV*VLRNLNLCNNIP*GLKVGEIQSPKAETKLGVERGGKNYIRFSK
916	6413	A	948	9	296	RPSHQCRLLPPRASLGLSELCPEDQ QSYIP*LGHHSACR*S/TSGGSCPLSVSSQASRAS/GPTSLTTAAPTSPRTGASALTEQYWSNRFLNHFAE
917	6414	C	949	114	383	MQMVGWVGGLGGIKQDKVLLSSEGPRSRDGGGTWRPTLKSTVRXXXXXXXXXXXXXXXXXXXXXXXXX SALL*
918	6415	A	950	1896	2251	IGTPLCRMEIDPFLEEAVPWSSVSSQASRASWPTSLTTAAPTSPRTGASALTEVGRPKT*DHKISSVSTK/TSSHCPGPEHTTSAVPVSRASSCPVTVTKL SKHPLQLARRVGFTLLY
919	6416	A	951	141	439	
920	6417	A	952	278	1177	RHPLAFFKASRAGPQRPLDGT LGPEDSRASSPMIQNSRPSLLQPQDVGDTVETLMLHPVIKAFLCGSISGTCSTLLQ\PLDLLKTHLQTLQPSDHGSRRVGMLAVLFKGVRTERRLLDLWKGMSPSIVR\VSLGVGIYFGHSLLF*SSISWRRPIPQTALEV\NHAGGSGSRVAGVCMSPITVIKTRYESGKYGY\KSIYAALRSIYHSEHGRGLFCGLTATILRDAPLSGIYLMFYNQTKNIVPHDQVDA TLIPITNFSCGDICWYSGPHWVTSTC

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						GMFIQNSYGRLLFHLKVSMDWPST
921	6418	A	953	109	376	SLTRAKSHLGQQFPTSRTSQEENWS P*RGSRTPPTPHTLPCQNLRPSMPT/F *QVNFQFRGAFLSG*KSSVAIRTIQ QSNMALMGTYAL
922	6419	C	955	123	329	MISRAPLPQLSELHCDKLHVDPENX KLLGNVLVTVLAIHFGKEFTPEVQA SWQKMVTAVASALSSRYH*
923	6420	A	956	41	565	APSPRRPWGHFTEED\KAT\TSLWG K\VNVE\DAGG/EKTPGKGPLVVLPP WTPEVPLTSFGNLS\SASAHGQTP KVQGTMAKKVLTSLG\DA\TKHL\D DSQGAPFAQA*SELALVDKPAWWD PE\NFKASWGNVLVTRFGQSHFRA KNFTPEGCRVSLGRKMGDLELASA LVPSRYH
924	6421	A	957	1	1000	STRAPSPGPFSSKLAGAYKSWCRR DPRTHSAGAQAAAARSVPIRCAPT ASATMSHHWGYGKHNGPEHWHK DFPIAKGERQSPVDIDHTAKYDPS LKPLSVSYDQATSLRILNN\GHAF\N VEFDDS\QDKAVLKGGPL\DG\TYRL ISVFTFHWGSF*WDKVSEAYCGIKK KYAAE\LTLGHWNTKYGDFGKAVQ EPDGLAVLGIFLKVGSAPGLQKV DVLDSIKTKGKSADFTNFDPRGLLP ESL\DYWTYPGSLTTPPLECVTWI VLNFPFSVSS\EQVFEIP*TLTFNGG GVNPEELMVDNWRPA\QPLKNR\QI KASFQIRWSHSLYSK
925	6422	A	958	3	402	EELTMAGIFV*PTIPIVSL/SLFCH*V LTLNSGISPAGSPVLIFSTPEPKR*TS QGESRFHTFYLLKGLNR*I*HPSSS SSSSSSSSSSSSSSSSSSSSSSSSSS NRFLKPLQHSPLPPPLKPLTYAPNL
926	6423	A	959	1666	2187	NFPSSASPPPTDSFL/GLSSEAPSEHR SPSCALDPIFFQTLW**SFSFSSLNFI NMLKFVPLNKTTPPLTL\FPYLKQL ASLPIQSCFFF*DKILLCHLGWSAVA QL*LTATSTSWAQVMFPRSWAYRH APPHT/LASCFYFCRDR/SLTIFPRLV SNSWAQVILPPRPPKMLGIQA
927	6424	A	960	3	695	TQLLRRPAVFVGSAAAGIRRLWSA SSGHWCAPAAGRAHAPVPRLVRL GAASTAAPQDAQTGPQPMPRADCI MRHLPYFCRGQVVRGFRGLQASL GIP\TANFPEQVVDNLPADISTGIYY GWASVGS\GDVHKMVMSIGWNPY YKNTKKSMETHIMHTFKEDFYGEIL NGAIGDYLRPDDNFDSLQSLISAIQG DF\EEAKK*LDLPEHLKLKEDNFFQ VSKSKIMNGH
928	6425	A	961	60	569	STDLEELPTLGWF*KQELIILSCPFVS LTYRERLPANFFKFQFRNVEYSSGR NKTFLCYVVEAQGGQVQASRG YLEDEHAAAHAEEAFFNTILPAFDP ALRYNVTWYVSSSPCAACADRIKT LSKTKNLRLLILVG\RLFMWEEPEIQ

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						AALKKLKEAGCKLRIMNLV
929	6426	A	962	62	858	QLRWDSGARAWPRPACLSPLPQRL LSHSPSMAQKEEAAVATEAASQNG EDLEN\DDPQKLKELIPLPFEIVTG ERLPANFFKFQFRNVEYSS\GRKTL \LCYVV*STGARGGKVQASWGYLE DEHAACPLQKESFSFNTILPAFRPK PLAVTNVT/WGYVSSSPC\AACADR\ IVKTLSTKNLRLILVGRLFMWEE PEIQAALKKLKEA\GCKL\RMKPD FRILSWENFVEQ\EEGSKAFQPWE DIQENFLYYEKLADILK
930	6427	A	963	409	747	VILQAQGSPMGP*SLRAFAESERC QKQERLEPEEGRTCAAGLRGGPRV WWPLSSW\TGDLRPSARN*ILPAA PMMEERKDPAPAQPPWTS\TLPQFV SPEVLCSPPIENSHT
931	6428	A	964	1092	2338	RCYCSI*PCFHLFQLSFQILDPPVLGT TFL
932	6429	A	965	146	180	
933	6430	A	966	2	921	
934	6431	A	967	1	621	
935	6432	A	968	2	152	
936	6433	A	969	157	1203	NNSGVMPEMPEDMEQEEVNIP**G GFWVTGCHWGFLGRAVHKEFQQN NL/WHAVGCGFRRARPKFEQVNL\A DSNAVHHIHDQPHVIVHCAAERR PDVV\ENQPDAAASQLNV\ASGNLG KGKAAAVWEHFSILHLGSGFCILM GT\NPPY\REEDIPASLNLYGQTK\A DGRKGCPWRNHLGAAVLRIPILYG EVEK\LEKKCCCELLMFE*KCQFQQQ SQAQQWIHWQARGSPPHMSKDVA PLCARQ\LAERMLDPSIKGTFHWS GNEQMTKYEKGMCQLPDA\FNLPS SHL/RDPITDSPV/LGAQRPRNAQLD CSKLETLGIGQRTPFRIKESLWPF LIDKRWRQT\VFH
937	6434	A	970	1	508	NSNRQNGPPKKGERERASN/C/YPG APAAQAE/APLVPLSRQNKSTVETS NLKMLISFPKTLRGPEGWWHQG INPGSGAATLGPGS/SPQRPQS/IAAS CSMARRTFFAVSSNSFFLL/CFLCM GSSSGSQPSSSLKQKKHWAKSGSFS VGQWMKPASAIRSGVQRSPRRAS S
938	6435	A	971	21	351	VVSITKAPAYREVSVHNSCLRSNEG GKQPSHTKCLCNSNLLTQFKTKPI E/CWPEKTYMGSSSGSQPSSSLKQK KHWAKSGSFSVGQWMKPASAIRSG VQ\RSPPRRASS
939	6436	A	972	1	1011	
940	6437	A	973	2	94	
941	6438	A	974	661	2244	QYFKNPVGSTAVFEMDRLFISSGTA EMTSRGFQRS\CNNPPCSSMTGRR ANQIHHLTPDFS\LRELLPPK\KAGT WADCVSPPCGERDRCEGWADRHR

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						A/CSSPAKSPTASSQVI*KGFKATAF FSRGRSGQH VAPRLHLGLSNHTAV GKREYLARRFLSLYSVSSSTRSFTPF PQ*LRMAFVLSF*IVVCAIL*INNSN KIRKPCC*TVEEPGTLSPFSHHTQV MHLPKKKKTKKHNNKKTVL*GGT GVTDKPEAAQIQQAPGKVPQDCD SLNNMRSRHHHCGRLC\HANKAVSS SKRDTAFFLPHFSPGKPGNQNSKNE PPKKRERERSSH C/YPAAPAAQAEA PLVPLSRQNRSTVETS NLKMLISFPK TLLRGPQEGWWHQGINPGSGAATL GPGSSGQRPQSM\AASCSMARRTFF AVSSNSFFLLLVSF\AILFLALSL\SSF KKFNQRVNSS\NCFLD/TERKAQPG RNCFLC\SSMGSSSGSQSSSLKQKK HWAKSGSFSVGQWMKPASAIRLRG CRRSPRRASS
942	6439	C	975	597	683	MWFHVCLLVVIFFFYFLVHMKYLKC KFLG*
943	6440	A	976	224	290	MPPIPMPIAPVPFPFGPGFPP/VYFPV PLPLP/LLFPF*PLFPF*PEVSAKPVTL WSRKRQRSKGEKEGRGRGTGK
944	6441	A	977	3	1815	HFVPVSPEAAAAESTACGVTAKML SVRVAAVVVRALPRRAG\LVSRNA LGSSFIAARNFHASNTHLQKTGTAE MSSILE\ERILG\ADTSVDLE*NLGVS *SIGDGIAPRTWG*RNVAEEMVVEF SSRLKGYVL*TLEPDNVGVVVFGN DKLIKEGDIVK\RTGAIVDVPV GEE LLGRVVDALG\NAIDGKGPFGFQRR VGEVGLKAPGIIPR\ISVREPMQTGI KA VDSLVP\IGRGQRELIIGDRQTGK TSIAIDTIINQKRFNDGSDEKKKLYC IYVAIGQKRSTVAQL\VKRLTRCKM PWKYTIVVS\AT\ASDAAPLQYLAPY SGCSMGEYFR\DNKGHA\LIYDDLI QNKAVA*PVKMSLLRRPPGREAY PGDVFYLHSRLLERA AKMND AFGG GSLTALQV\IET\QAGDVSATIQT DV NSI/TLPEQIFLETEWFNKG\MRPAIN VG\LSVSRAGSPPTNPGAMKPGSQV PWKLELASSIREVACFLPPVSVSD\I DAATSTNLLESVA VPS*LEFAESQG PVFSPWLIEGTSCLLSYAGCKGDIFD KLEPSKITKL RNAFLSHVVSQH QDL VGALCRADGKISEQSDAKLKEIVT\ NFLAGFEA
945	6442	A	978	532	878	SYHFGRRPRQADHLRSGVQDQPGQH EETPSLLKRQK\LAGHGGIYL*PQLL GWL RQENCLNLGGGGCSELGLHHC IPAWATEQDCLKKQNETKKESYS** GTSCLIAFLFILKSDQK
946	6443	C	979	36	236	MGPTIPDXS\FFWRKPITWMPTWE GTSNVGPQPLSSSKSLHSXRGHPAPI PTGQAGPRDSGPGASP*
947	6444	C	980	26	160	MRFQSTGLGAPH CALNKC VSC LN X XXXXXXFLLRGPKLNPFKGG*

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948	6445	A	981	1	523	FFPKGFFLGYPRVFPFPFLNPGPGQ I*FSPP*K/RKLRAP*KKASSSSSVK TGNTFIESTVGCAPCALEPHHSAP/ PQQPAPSGPGPPGEPG*ERLCASHK AFISHKQSH*SPO*PCQAGVTL SRLQ TTNSPRP\PVRRGCGGLEPRP*VS/PS QPTACSENSQGSQSPSKRTLS
949	6446	A	982	145	1315	CLPPPGLGPAPSLSSSCWGPPMPRT IRGIPPGSICRLCFCPAAGLLSLVAL QRPASSPTRHSALLCLLRWA*PTSPS LPQSLGSRAQLHSPLP*QAGSPCHA HTCGHLGPPVV*VPLPCPRSHSHSS CLFPAGSQCP*QAPAGVSISCQASSS ASSCGPGPQGYGQTPGPIPETPRDR\ PCHPTPPKSKLQARGPWRAWVG*R TADGSCGKKP*/CGPTIPDPKSSPLA GLSSPPFWFWAETHHPGMP*RGKR DPRKCGNPQPPSPKLRKSPPTAHGD HPAP*FPTGKGWTPKDSWTPGPPP* SRRPRPLN*WTAA*PWGQNPWAWT PAHPRKKP*RPRGSCLSLSVSACGK WAPSPTSQGCCEGRCDVAVPKQQGL AHPTVLLNKCVCVSLN
950	6447	A	983	1	682	PPLFFQAAGKMADIQTERAYQK\QP T\FQNQGRGSCCGETGK\EKLPR\Y YKEHSGGLQRHPKEAY*GPPTLTK KCPFTGKCVHFEGGILSG\VVTM KMQRITIV\RR\DYHL\YIR\KYNRLP RKRHKNSMV\HLSPCFQGTSRFG\DI VTGGAKCRPSEARQWRFNVLKGH QGLARHQRSSFQKFLRLGHRGRSPT MEIRLVASPGKKKKSFVPTGGAV DSIGGRGV
951	6448	A	984	1	465	
952	6449	A	985	1585	2239	
953	6450	A	986	9	2580	SLPPKKCELRLHNCWGLFSPPARQ SGSVA AVVAASAVSGVSGPQSPLT CASSSLRSPRPARTRPVAVCVSPTTP RLPPRSSLRADMSGDHLHND SQIEA DF\RLMDSLKHKD\KQKDENARAR GHKEEKDR\EEKHSNSEHKDSEKK HKEKEKTKHKDGSSEKHKDKHKD RDKEKRKEEKVRASGDAKIKKEKE NGFSSPPQIKDET*DDG\YFVPPKEDI KPLKRPRDEDDADNK\PHKKIKTED TKKEKKRKLEEEEDGKLKPKNKD KDKKVPEPDNKKKPKKEEQKW KWWEEERYPEGIKWKFLHKGPFV APPYEPLPENVKFY YDGKVMKLSP KAEVATFFAKMLDHEYTTKEIFRK NFFKDW RKEMTNEEKNIITNL SKCD FTQMSQYFKAQTEARKQMSKEEKL KIKEENEKLLKEYGFCIMDNHKERI ANFKIEPPGLFRGRGNHPKMGMLK RRIMPEDIINCSKDAKVSPPPGHK WKEVRHDNKVTWLVSWTENIQGSI KYIMLNPSSRIKGEKDWQKYETAR RLKKCVDKIRNQYREDWKSKEMK

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						VRQRAVALYFIDKLALRAGNEKEE GETADTVGCCSLRVEHINLHPELDG QEYVVEFDLFGKDSIRYYNKVPVE KRVFKNLQLFMENKQPEDDLFDRL NTGILNKHLDLMEGLTAKV\FR\T YNASITLQQQLKELTAPDENIPAKIL SYNRANRAVAILCNHQRAPPKTFEK SMMNLQT\KIDAKKEQLADARRDL KSAKADAKVMKDAKT\KKVVESK KKA\QVRLEEQLMKLEVQATDREEN KQIALGTSKLNLYLDPRTVAWCKK WGVPIEKIYNKTQRE\KFAWGHLT WLDEDEYEF
954	6451	C	987	65	235	MQFRVKYHICSTLLSLKTKICITCIP SHLFPASTIPSWGCFHLYIHIAQKHV ING*
955	6452	A	988	16	148	SPAEQGCVCVCVCVCVCVCVCVCV CVCVCVCVCVCVCVCVCVCVCVQV ACVCN/CVCVCVCVCVCVCVCVCV CVCVCVCVCRWVLACATCVL
956	6453	A	989	287	504	LPRNFKTIYLDSEMVLESSKRGVCV SVCVCVCVCVCVCVCVCVCVCVCV /C*YLDLNHGKCTHPVSFSVRIFLA
957	6454	C	991	201	488	MGSRPRFCLFTNTLCPDVTSSVC SPKTTXRRLKXTFMPRCRKPQAVL TSSEMALAACSXFSRSPDDFTQYQV AELVWDSLQPLGQXRSHCSLR*
958	6455	B	992	53	302	MTSALTQGLERIPDQLGYLVLSEGA GLASSGDLENDEHAASAMSELVST ACGLRLHRGMNVHFKRLSVVFGEH TLLETRVLTEX*
959	6456	B	993	277	573	TSALTQGLERIPDQLGYLSSGDLEN DEQAASAISELVSTACGFRHLRGMN VPFKRLSVVFGEHTLLVTVSGQRVF V*
960	6457	A	994	134	1271	NPGPVQVGVEGGQEEGPSSKKQAK TRQVCLASITEAPGPKIRFSEPLRPP AGCRHQMGSPSTSGSASSPQTPFCPG/ PPSPAVCV/PPKTTGGETHQTGA*RA HSMPCSRKTAGCAEQLQRWHWL PAHHSPPQMTPALHLHSVPGSRA GLGFAPAPGSAQKSSG*RCKS*EAC *RDGRPDTLHLQTQVSGLT\WPQVF SFPSQVPSRPPPPYMLNTDLPÉPPS APTLAPRLPWPSTSHLCYPKGPVLP LWPLPSDP/SSPPFVSARPA/ALPAAP EHPPTDPSPAFSSPSLPPSPLPPRAD RR*GWSAGPPGG/EPHRLGSRDAEP PAGPLAHASSLTIAVFGAGGAPYQI GSFRLQAPVTCLQPLRSSFCLRHWP LAPPLA
961	6458	A	995	1	422	
962	6459	A	996	3	760	TSRGRVGTQAGEPRDLRPPPCPSSPL RV\AVV\CLEQPERGAWEAHNIPQP NGDSA\VRSG\TGTHVKLPGPAD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGR\NRKRIK\GPERF

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						QNCKDLFDLILT\CEERVYDRVGWK I*ISR\EQGDLPSPVHVVNLDIQDNH EEATLG\ARFLICEVCQCIQHTEDM\ ENEIDELLQEFEEKSGRITFL\HTV\CF ILFSFLDICF
963	6460	A	997	425	591	EYLKQWNVVFVDIKNHL C/MHLHA HIHTQV*THTQTHTRHTHTHTHTP CHCLVHTA
964	6461	C	998	120	368	MGTAKHPGYPQISTTVCIYVPDFAIL SPVLSFCRLIYLHTRMLQATELLQ ALQNSTTKGNRRERARDNSKMRH DGRAWR C*
965	6462	A	999	2	393	ARGKKPNLRAFLPLPRAWPEPQTL QQPRWP*TVQLPVPAIGDKALALGR RKSGPGPGFVVLRTVPHALSHVRS FRSLLLPLSLTLCVSFSFCLSVFPSPL PCSDGANPWQSQSWKQEDGSSSPW EVSA
966	6463	C	1000	1247	1716	MLRPRLRCFFSSSQTACSSDLNRSV GSSQARPQGGSPSSFSASCRKCSSVLH KEGPQLLVVGQVPSFYGPSTCPFHT AAADSAWPCRSRASFKVLSHDFHR PLVLLAAQRLPPARFPLGRLGARSH TAGGAERAGVGAAQQLQRRPRWP GRRARAPRP*
967	6464	A	1001	3	630	FCPRGQEFGEKNLLSPRRPWGHFT EEDQGLLSTSLGQG*ILEDAGRKK PLGKAPLVV\YPMGPQGFL*TGFGQ PCPSCPLPIMGQPPKVQGHMAKK\V LTSLGEMPIKH\LD DPQGHLCPSLSE LHCDK\LVDPENFKLLGKCAGD\V FGNPFQRHPWRLQASWQKMAED GDCKWPVPCPPDTTEASWPMNSEA FKDKAFILASNYK
968	6465	A	1002	41	625	APSPDAHGVISQRRKATITSLLGQ G*ILEDAGGRKPLGKAPLVVLPKW DPKRSFEQALGNPVPLPSA\IMGQPP KVQGHMAKEGA*PSLGEMPIKH\LD DPQRAFAPA*SELH\CDKL\HVDPE NFKLLG\NVLVTV\LAHFGKEFTP/E RLQASWAEDG\DV*SGQCPVLQIPLK PLGP*IQKLSKDKAFILASNYK
969	6466	A	1003	106	1315	KQSGRAPGKVVSRAFPGLNPCPGW K\LLTQ\VGAVLGRGLGALG PGNRTHIWL FVRGLHGKSGTWWDE HLSEENVF\IKQLVSDDKAQLASK \LWPLKDEPWPIHPWETGSFKVGL FDLKAGHVGLLWTKDGQKHVVTL LQVQD\CHVLKYTSKENCNGKIGNP VC*EGKTVSRFRKATSILEFY\REL LPPK\QTVK\IFNITDNAAIKPGTPLY AASLFVQGGYVDVTAKT\GKGFQ SCSLKRWG\FKGQPAYRIGQTENPT GRPGA\VA\GDIGRVWPGTKMPGK MGKHIHGQNMGLK\VWRINTKPII\ YVNGSVTWDIKNCLVKV\DSKLP\ AYKDLGKNLPPYIIFLMGDGRGNL PERFCID*KPCCQPRWRPPINICPNIL

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						WDVGRTLTIPL
970	6467	A	1004	218	530	KFEGCLPPRDETRIPWARRCAYVV *SKEVSL*HCNTVTPG\GKPNK\TRVI WGK\VT\RAHGKPVAMVRAQIPEG NLSCLRPFGRH\IRSDGCYPSRILNLT EKS
971	6468	A	1005	2	269	FESEDEGEEDD\WEDDYDYPEEEQ LSGAGYR\ADKMFLRTREPALDGGF QMHYEKTPTFDQLAFIEELFSLMVVN RLTEELGCDEIIDRE
972	6469	A	1006	1	456	AELSELYEESDLQMDVMPGEGDL PKWEEATGTRAAIPWVPPATGAQQ LEEEGPMEE\EEAQPMAPPEGRSL ANGPNAGEQPGQSPGRRTSRAEDE A\EEFDDWEDDYDF\PREEPVKGAR LRFLPPS*KTPPSFWENRNTPLWGG LKIFY
973	6470	A	1007	563	771	WSMVSLCSTAAVAPVCSRIPTERR ATASVTHFCGDLG*SPVKPLSLGYR SNLGGPEEGREGGRKARRK
974	6471	A	1008	300	391	AVCTMSEMAELSELYEESDLQMD VMPGEGDLPQMEVSGSRELSLRPS RSGAQQLLEEEGPMEEEAQPMAP EGKRSLANGPNAGEQPGQ\VAGAD FESEDEGEEDD\WEDDYDYPRRR SQLQWCPVTRVSAALEEA\DKMFL RTREPALDGRVSRCH\YEKTPFGSV SLLSEELFFT*LVCQSV*PEEL\GCDA WRG
975	6472	A	1011	100	270	LRSSAVTVLVSLIHSPSSFAHHPVSD T*PHCLESPPGFKAIFIRGRLFTEACF CRIA
976	6473	A	1012	13	670	RQRPKARASIPHLQPPQEACQPPAA ALTRPQPRP/PSALSHPAKPHSVSSA GSSYKNNPFASSISKHGVSSGSSSSG GTPVQSSVSGSLVPGIQPPSVGQATS RPVPSSAGKKMPGFPEVDSGSPSRR SK\GDSSGGTQGVAKLLTSPSLKPSA VSSVT\RLPPCQKERVGLCCWPAPL *WLHPTNPAAQSCGLP*ARTPRGLG AAGVSLAQRKSLSTYRA
977	6474	A	1013	3	578	GIPWWTHASEAVQTEIPVVGPREW QSC*PRR/RLKPSAVSSVTSSTSLSK GASGTVLLAGSSLMASPYKSSSPKL SGAMSSNSLGIITPVPV\QCSPSAL TPLPKQGSPPMPSSQALPPGPSTRP WPQSSGWLALQAPCASPTRCGA HPYPAESAR*SPDGQCAHAHRVPLP SPPLGALPLPRVLVSLP
978	6475	C	1014	426	653	MVTWGGGSHQRRERKEGPGTRVFM GREALESPCSASHCRPLLGFELSNT NLLLWLFYLLRLLCKQTGNPSCK KYI*
979	6476	A	1015	1286	2318	RTVPFYPMHLMVMMKTEPKIGVCK NPIIVESTKVFSKELHCHVPREKL APTIVST/PLGVLSISQGCSPSCGS/ GPEFCPL*AHSLGMGRHWDHPGSL

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						LQPEGAPEQWGALRYSDQMPGDQ ADSPTGVPTALPPEPVNTVPPTTAQ RKPQPRAAPLTTV*QSCKAQSTGQ SAPPEQQGPGSLHGRHIRSAEKRSA ENSRSSRRTPSSRKGA VSVHPGRPA RSDS\PRPKWQALPLKRSQFPWYSR PFPVKLRSTWKRVRKIRTQVFHAL* FP*GSSNQT SRETPK*QKSPNAECSR AQTSHETPASSYSCTLLLATACKHTI TVKVGGHSAQCFQNSNSAVQL
980	6477	A	1016	315	480	
981	6478	A	1017	1	1845	
982	6479	A	1018	1	447	
983	6480	A	1019	218	544	SGFSLSLRGSISFSL/CFKVGMCVTY PRCYC*\SVPV*KPLIKPGWSELKPK MNWASCSR TLASFLQAARSHPW PMKMETMEQSKLRSQPCKPAAGAV DPRAVVHGT
984	6481	A	1020	198	562	LKCGKQWSDPITSPQTESQLLGSSQ QQLHQQRHLQGP*K*NRDSPLCFSL SSCPIPKTYTNRHILLP/SSSKSLCKF L*PA*ISPQKMGFSFLSQSVCKFSKL LCSASLIKLFKAFNSIQVTS
985	6482	A	1021	72	270	
986	6483	A	1022	545	812	
987	6484	A	1023	477	750	
988	6485	B	1024	537	867	XEQAAPCSALSLPMASCLRGHGEA RADPWSSTRPIDLKFKGPFTDVVTT NLKLRNPSDRKVCFKVKTTVPHRY CVRPQQWNLLTPGSTVTVSVMLQP FDYDPNEKSKHKFM*
989	6486	A	1025	822	1750	SSAEPSPSPSPAPSQQTAAAGAPPLC AVSPMASASGAMAKHEQILVLDPP TDLKFKGDG*VFIRPEQYYTV*KWC KRSKRHGPFRPFTDVVTTNLKLRN PSDRKVCFKVKTTAPRRYCVRPNS GIIDPGSTVTVSVMLQPFYDPNEK SKHKFMVQTIFAPPNTSDMEAVV/W KEAKPDELMDSKLRCVFEMPNN DKLNDMEPSKAVPLNASKQD\GPM PKPHSVSLANDTETRKLMEECKRLQ G\EMMKLSEENRHLRDEGLRLRKV AHSDKPGSTSTASFRDNVTSPLPSLL VVIAAIFIGFLLGKFIL
990	6487	A	1026	184	282	VIASQNIFVLSSVTGPKDRSGRQPLV FLKSPG*THPS*SVSRNLFS\FA*PGD FRKTGCRPDL SFGPVTLLRTKIFW LAIT*D*CFLGYIKMGHIVEHCQQ
991	6488	A	1027	445	992	HCCGRNCLQRRWGWRVRSLLAGI VFVSPFFKLELQKPLPSEQITIGLML LPFPHFFFCFVFCFLVCLFF*DRV MLCHPGWSAVVRSQLTVTSASRVQ AIICLSLPSSWDYRHPPCLAFSR/DR GFTILARLVLELMTS*ATPSLFCCFI ADSVQQYAPSLYILRNTNPRLLAK IFVA
992	6489	A	1028	33	476	HEDHAGPEPPRSYIPPYNATVVQKL

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						LDQGALLMGKTNLDEFAMGSGSTD GVFGPVKNPWSYSKQYREKRKQNP HSENE DSDWLITGGSSRGSA AAVSA FTCYAALGSDTGGSTRNPAAHCG V/GFKPSYGLVSRHGLIPLVNSMDV PG
993	6490	A	1031	187	1611	RAWERQERQSRGCSWLTRGVRRG GEGRTTRRKMASKEMFEDTVEERV INEEYKIWKKNTPFLYDLVMTHAL QWPSLTVQW/LSLKVTKEGK\DM LHW/LGLGTHSD*SRILVVARVHI PNDDSQFDA\SHCSDSKGEFGGFGS VTGKIECEIKIN\HEGEV\NRAR\YM PQNPSHPLLTKTPSCLMVLVFDYTK HPAKPDPSGECNPD\RLRGHHKEG YGLSWNSNLSGHLLSASDDHTVCL WDINAGPKEGKIVDAKAIFTGHS VEDVAWHLLHESLFG\SVADDQKL MDM/WDTRSQYHLPRPSSLGWD\A HTA\EVNCLSFNPYSEFILATGSA\D KTV\ALWDLRNLRLNLHTFESHKD EIFQ\VHWSPHNETIFGFKCTCRR VWDL SKIGKEQSPEDAENGPPENLL IHEGH\QVKISDFSWDPPMKPWVICS \VSEDN\IMQIWQNGLKIFYNDERVR CHDHPKLEGKGS
994	6491	A	1032	3	551	FLLAPVEVSEGSFAEIWGQITGVGLF LCLGES PACWERGLSKRDLMSVKA CGPKAHFCLGYKAGGLPGTQRGAT QALL*KFEGVYARRMKPDSNLGRR CAYVV*SKEVSL*HCNTVTPG\GKP NKTRVIWGKSKLGAHGKQWAWF VPKFPKAIFFA*RPFGHR\IRSDGCYP SRILNLTEKSN
995	6492	A	1034	20	867	ALERRVRKSGDCCTDSGTMNIFDR K\ITFDALLKFSHITPSTQQA/HMKK VYASFA\LCYFGAAAGAYVNMVT HF\IQAGL\LSALG\SLILMIWLMATP HS\HETEQRRLGTSLLGFCIPYRKL LGPALGSFVIAVKRQASLPTAFMGH SNGSFPAFTLSALLC/RRPRS YLFLG GIL\MSALSLVAFCLPLG\NVFFWIPF WVFQA\NLYVGLVVMCGFVLFDT QLI\IEKAEQGDQDYNL/WHC\IDLFL DF\ITVFQKNSMKDPGP*MKKDKKK RRRNEVTIQPFI
996	6493	A	1035	153	546	PAQETGRPRSKAHVASTWRAFPPE DQVLLAGAP/LWEDEAHFWAKCG VEAL\TTLEVTRPACLEGK\VHGSL ARAWKSDEGQTPK\VAKQGERKK KTGSG*/RRPDSSYNRRFCQTLLPTF GKKEGPQWPTS
997	6494	A	1038	1	433	
998	6495	A	1039	101	1898	SAAMIGGLFIYNHKGEVLISRVYRD DIGRNA\DAFRVNVIHARQQVRSP VHQHLLRTSFFHV/IRRSNIWLGSSS PRQN/VSTVAMVFEFLYKMCVMA AYFGKIS\EENI\KNFVVHYMELLD

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						EILEFGYPQEFRD/SGALKTF\ITQQG IQGVQAS/AQKEGSSQFTSQVTGQIG WRREGIKYRRNELFLDVLESVNLL MSPQGQVLSAHVSGP/VWVMKKNYL SGMPECKFGMNDKIVIEKQKGTA/ G*NQARAGKQSIADDLHLSTQCVR LS\KFDSERSISFIPPDGEFELMRYRT TKDIILPFRVIPLVREVGR TKLEV KV VIKSNFKPSL\LG\QKIEVRIQPLNT\ SGVQVICMKGKAKYK\AGENSFVW KIK\RMAGM\KNTHIIEIGFLPNKEK KKGGCPPLFPRNFGFKFAPSGLKVG \YLK\VLNPKLNYSDDHVIKWVR* GR\SGIYENSACKATRQLAQLPQPPF LQQVQVPLLPTTHQVSPSPPCFAC PSPLQPSPEVLGLGQSNITKWDRWK QPLGSPGQGSSEGSCSPHPVCSWP NAQALSSVTQSPGGFPFLPHPCGHS SGVGGVLVAPHLRAPPKASEWIPGLS PYSALG
999	6496	A	1040	255	662	TGEGYAGTEATDITHPQLRNQQWV PRCKPFPICDLKIOPERNYLFLLR/QR VSLCHPGWSA VV*SRLTATSAFPGS SYSPAFSLPSSWDYRCAPPRPANFCI FSRD/RGFTMLARMVLIS*P\VIHPP WP\PKVLGLQA
1000	6497	A	1041	2	297	TLILPQHVNCPPGINA WNTITSYIDN QICQGQKNLCNNTGDPEMCPENG CVPDGPGL/VLRDSGSHHSIRLHSA/ LGDPA PKSQDFMNYIGLTIDLRSI
1001	6498	B	1042	1	786	MAPHDPGSLTTLVPWAAALLALG VERALALPEICTQCPGSVQNLSKVA FYCKTTRELMHARCCLNQKGTIL GILPQHVNCPPGINA WNTITSYIDN QICQGQKNLCNNTGDPEMCPENG CVPDGPGLLQCVCADGFHGYKCM RQGCLSAAPQALAGKWPPKNCHL PSFVDGQPQGQKEPCNNYPSIYTFV PVCQGICGIKMLKTELLHLKYWDIG PGNRNSYKFAAGNVKFAVTLNSL LIPQKAKRNYHMTQQFRS*
1002	6499	A	1043	137	1021	GRAEAGSLASQCVASGSPVLLG GPAVLISLTLDPDAQPDMHPMSRE RAKFVKSGL\YCKTDTKS*CLHA\RC CLNQKGT/ILWGLDLQN\CSL\EDPG QNFSIRHITTVI\DLQANPLTGDLAN TFRGFTQLQTLILPQHVNCPPGINA WNTITSYIDNQICQGQKNLCNNIT GDPRKCVPEKGILCYLNGPKVFWQ C\VCADGFHGIQSVLPGLVPHCL MFLREFWEPTHSIRL\HSAFGGPSA* KAKDFHGTYIGSLPFDLKLINLELSA PVRGALLPRKGIFRPVGFRLLKG
1003	6500	B	1044	203	308	XRPLFAPVRARAVEAAGPGSGRAA EHSGPTGTAGCA*
1004	6501	A	1045	78	308	
1005	6502	C	1046	35	259	MQFSTHRGQKYERTPDTS GARVIER PYLTVIIHNNLEGRLLKEKSGKPYKF

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						AFYVILRCHFTDNFTTAALFVTR*
1006	6503	A	1047	162	1341	PPFQLIMGEIKVSPDYNWFRGTVPL KKIIVDDDDSKIWSLYDAGPRSIRCP LIFLPPVKWNCKMSFSRQILALTWM GLTGLIAFAVIPVYCDHLEFCDGFR KLLDHLQLDKVHLFGRFFGKGLWP MRFTGIPLQIS*SPIPLILCNSLMDTS IFNQTDCKQLLA*CPAFMLQKNSS LG\IFHPGPGGPYGWAGCHLDFHG* DRA*ESFGVQELNLAFAQGLTLELSK FLCGNLH*NSGTYL*TIYGMCLDPG GGAFLQLKLLKKWYKLYPNGPKKL HLKTGGNFPYLCRSAEGLNLMVQIH LLQFHGTYKAAIDPSMVRPRSLRC RKAALASARRSSSVSSSPVNDELTP VCSLYSQWAFSTRSDRPFPQVPSG LTRGPHWGLGKVGLDGHL
1007	6504	A	1048	321	888	VELSVHPIPADPRSLLAGAMPWKL PISLPAE\PPCSLSCCLLPATQHPLH PALPAVDGAKKNPVFSGRLPPP/PT QRTSASGISALYA*DREV*AQISELW AMRG*VQKVGTVQISRAGQLAAV TSVGNMSVYPLALMTPPPSPPLPP PPPPVGRWSVGLRDLSPA VPSSEV CLWRSVLCLIPGY
1008	6505	C	1049	137	320	MLKSSFTCFPTEKGPKFLEDNLKTK XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXLV*
1009	6506	A	1050	231	477	GVYFIFIGLVVFCFVLFDDGRFTVA QAGVQWCDLGS LQPPPP\GSNDSP WPQLPE*LGITGACHHARLIFIFLLE TGFRPC
1010	6507	C	1052	60	523	MAEAGFIHCPTENEPDLAQCFFCFK ELEGWEPDDDPMQRKPTIRRNLR KLRRKCAVPSSSWLHGLRPLRXLP PRVAAPLPGFIPWCHQPSGPLSNV LGKEINIFKLDVSTVLLFCLESGRG VLPVQRVLLVQLLALSLSPPFFGGPF WRFE*
1011	6508	A	1053	61	208	IFETGQRKSQEQNWSYSVTQA/GVQ WCDLGSPQPRPPGLK*FSLHSYMG
1012	6509	A	1054	198	1011	QTHGLQPSQHLPTSTLRTVTAST/ SMRSRHHHCGR LCHANKAVSSSKR DTAFLPHFSPGKPGNQNSKNEPPK KRERERSSH CYPAAPAAQAEAPLVP LSRONKSTVETSNLKM LSF PKTLR GPQEGWWHQINPGSGAATLGPGS SERPQSIEASCSMARRTFFAVSSNSF FLLLVSFAILFLALSLSFKNSPRVNS SNCFLTERKAQPDECFLCSSMGSSS GSQPSSSLKQKKHWAKSGSFSVGQ WMKPASAIRSGVQRSPRRASS
1013	6510	A	1055	1077	1457	ARRPEPPHPAHRRGGGTPAQGGAG SPGASSDTSLRLEAPPQSIACWRSCC NAASWWTRSRGTC SRQTQR*GWP* CWRAQRGCAPALAAPQFLAAHHG QRSAAASTTPGLHAGLRRSRPPRP PRP

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1014	6511	A	1056	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHA W\FFFFCS/RD TVSLCYPGWSRVA*SRITATSA\PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGSLCCPGWS* TPELK
1015	6512	A	1057	166	409	WSDVVGTRHLSAASFNSHAFWNLE EELTLVKGQALPSRGLDCPGRPAPP AACPGPKWRACLWV*FPNQNPISPG RNFNLKT
1016	6513	A	1058	10	604	ARPPKKPTSPTATTTTR*GARPATPP PRRPTAPIRWPCPTSTAPPRACI*AT AP*QPQPAPHQQTAAALFWASPPPSH QAPWIPPFLQPPS/LPPPPHSPRGP PGAQQGGAPAEKPWRPWTAAQR*D WTPPGAGLELGGSPGLWGHRRARE GGAGEGRGFPEDRTGRFYKRIFVGR GDSKLPGPRGSFRSFSGKFFLCF
1017	6514	B	1059	167	355	MASGSNWLSGVNVVLMAYGSLV FVLLFIFVKRQIMRFAMKSRRGPHV PVGHNAPKRSHFILK*
1018	6515	A	1060	67	458	
1019	6516	A	1061	164	528	
1020	6517	A	1062	203	364	
1021	6518	A	1063	103	1019	GNGRGAPGDPCAVASAEPGLTSQD SGVNPNNNSARGREAMASGSNWLSG VNVPLVMAYGSL/DVCTAIYFCEEA NHALCNEISKGTSCPCGTQCPQGT* K*EIDIRLSRVQDIKYEPQLL\ADDD A\RLLTGKPRGNQSC\YNLVIGM\ KALGLPFRTS\EIPFHS\EGRHSPFP* WGKNFRSYLL\DLRNTSTAFQGCTA KHLIDTLFGMAMET\ARYGDKGVF WPRMKYLRVQEALSELATAVKARI GELFSDIH/HVQAAKDLTQSPEVSPT TIQVTYLPSSQSKRAKHFLAELKSF K\DNYNL\AESTL
1022	6519	A	1064	1027	1365	PEVNRLYCLFKNKI*KALLSFQTYIC IYVLDVLIKEMVFKMCQVVVCV\VC IYMCVCVCIH*CVVCVCIYHTHTHT C/VCDW*AIQ**TCPHYFFLILDQCC PNCTFPLMVTML
1023	6520	A	1065	675	819	HRLDRAHP*RAEGNCLLPVYLSY/G PLIA*TGQGTSSPCLCSL/*PRSAITHT PSQPGDPRQPQTVHSGELNPRVYTK
1024	6521	A	1066	3	603	VDDFVQPARRRWEMLGVLPSVFLG LRRFVHPAKGMKQTRGDSFAFQSG

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						SPGVCFEGQEAEGSLSYGVGLIAAG FVLLSPPSQC/HDSLATQVLVCGVA LLWPSSGRAGTVQP*PAPENRSASP FCLPGHIQVPVFTVPRSAITHTPSS NLGTPRQPQTVPPLRGAESPGQPCPM SLRKLPQARPLVLYTCSCHPAVDEC FR
1025	6522	B	1067	46	1983	MRPRKAFLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLIFYAPWCGHCKQF APEYEKIANILKDKDPPIPVAKIDAT SASVLA SRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKE NFDEVVNDADIIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDYNPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVIIIIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQGQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSA IKDFVLKYALPL VGHRKVSND AKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEVAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFFKKGKLPVIKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDV LIEFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVI AKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEEL*
1026	6523	A	1068	1	849	
1027	6524	A	1069	74	2705	KKLDFFRSLPVFQADFSHWQLFRVL FLLHPPLVISMDSWFILVLLGSLIC VSANNATTVAPSVGITRLINSSTAEP VKEEAKTSNPTSSLTSLSVAPTFSN ITLGPTYLT TVNSSDSNDGTTRTAS TNSIGITISPNGTWLPD NQFTDARTE PWPGNSSTAATTPETFPSPGNSDSK DRRDETPIIAVMVALSSLLVIVFIIIV LYML/RGFKKYKQAGSHSNFRLS NGPH*GMWEPQSVPLLA RSPASTNR \KYPTPGPWDKLEEEINRRMADDNK LFREEFDALPACPIQATCEAASKEE NKEK\NRYVNILPYDHSRVHLTPVE GVPDS DYINASFISGYQEKNFIAA QGPKKETVND FWRMIWEQNTATIV MVTTLKERKECKCAQYWPDQGCW TYGNIRVSVEDVTVLVDYTVRKFCI QQVGDMTNRKPQRLITQFHFTSWP DFGVPTPIGMLKFLKKVKACNPQY AGAI VVHCSAGVGR TSTFVIDAM LDMMHTERKVDVYGFESRIRTQR* QMVQTD MQYVFIYQALLEHYLYG DTELEVTSLETHLQKMYNTIPTNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NGL*EEFKKLTSIKI\QNDKMRTGNL PANMKKNRVLQIIP*EFTRVIIPVKR GEENTDYVNASFIDGYRQKDSYAS QGPFS\HTMRDFWRMIWSGKSCSIV MLTELEERGQEKCAQYWPSDGLVS YGDITVELKKEEECESFTVVRDLLVT NTRENKSRQIRQFHFGWPEVGIPS DGKGMISII\AAVQ\KQQQSGNHPI\ TVH\CSPGGKERTGTFCALSNVL\AE RVKA\EGILDVF\QTV\KSLR*\QRPQI GSRQLEQY*VLAYKVVPGVILDAP QINAQLQSKAANKGPVDPGGLPFNI LVIFLFC
1028	6525	A	1075	734	1151	YRRGPGGLRWAEMSGDFPPIPLPVR GIHPIPLRASQ/PVL*GGQQGMGTGP ISQ/PGETEFQTGLSACPKPHRVP SSCTTEKPSQRLHEQMVRGG*SSMG GAGNGVGMESGTVQGTSPSGSWR PAGTGVGARNCWYLPL
1029	6526	A	1076	118	399	
1030	6527	A	1077	1	214	LLMRVSLPSEVFFCVVFETESRFVT QAGVQWHDGF*QPPPPRFK*FSCL SPPSSWDYRHVPCLANFCIF
1031	6528	A	1078	2	152	ETESLYVTQAGV\QWHDLSLQPPP PRFK*FSCLSLPSLTTFDTSLKSME
1032	6529	A	1079	2	426	
1033	6530	A	1080	1	1716	
1034	6531	A	1081	2	886	VGGRGEALDGGGSGAPPSVSQTES RAGTMSAYPKSYNPFDDGDE\EG ARPAPWRDARDL\PDGPDAPADRQ QYLRQEVLRRAAATAASTSRSLAL MYESEKVGVDSEELARQRG\VLEA HREDGGTRLDDQDLKISQKHINSI*ER VLGGLVN/YTFKSKPVE\PPPE\QNG TLTSQPNRLKEAISTSKEQEAQYQ ASHPNLRKLD\DDTDPGPPEAWASAP GV\MLTPKNPHLRA\YHQKIDSNL DE\LSMGLG\RLKDIALGMQTEIEEQ DDILD\RLTTKVDKLDVNIKSTERK VRQL
1035	6532	A	1082	1549	1712	SNL*FFFFEMESRVA\RLAECSGVIS A\HCNLCPLGSSNSPTSAS*VAGITG A\THHSRLLFVFLG\ETGFHHVG\QA GL\DSLTLMIQPALASPKCLGLQAVS PPMPSPYSSSFFCPLNLT\PHVLYPG LNPPSSFCSDL
1036	6533	A	1083	2	336	
1037	6534	A	1084	218	1080	PSSRMNH\LPEDMENALTGSQSSIAS LRNIHSINPTQLMAR\IESYEGREKK GIS\DVREDFCLFVTF\DLLF\VTLLW D**EFKC*MGGHLRNTFRRR*LQY *LTISSIFLILFLPGQFFRF*KCLILAY A\CR\LRHWWGQ*RLTTAMTSALL LAKVILLKLSSQGAFGVYVLPFI\SFIL AWIETWFL\DFKVL\PQEA\EEENR/L SLIVQDASERAALI\PGWSFWMGQF YSPPGIRRQDLEGLSKEKQGLRKP

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						LFRNYEYYFLFKCGKLTESHGKKRQAVESPCRQ
1038	6535	A	1085	3	400	
1039	6536	B	1086	333	436	XTPVFSYGDEIGLDAAALPGQPHEGLLLRFPYAA*
1040	6537	A	1087	127	2041	RGVWGGHVPGGSSREEWSGEDQGGKRRGDAVAENCAEAREAGESVLGPRVQVGVEPPSDRKLRRVAGSAGTM SQDTEVDMKEVELNELEPEKQPMN AASGAAMSLAGAENGLVKEIFPQ KKKGGGSAEDEAEAAAAAKFTG\L SKEELKLVAGSPGWVRTRWALLLL FWLG\WL\GMLA\GAVVIIVRAPR\C RKLPAQKWWHTGAL\YRIGEPLRP FQGQRRGANLAGSLKGRLDYLLSL KVKGLVLGPIHKNQKDDVAQTDLL Q\DPNFGSKEDFRSL\HSVKTKNL RGILD\LTPNYRG*ELRWSTQVDT\ VATKVKDALEFWLQAGVDGFQVR DIENLKDASSILGLSWQN\ISPKGFS E\DRLLIAGTNSSDLQILSLLESNKD LLLTSSYLSDSGSTGEHTKSLVTQY LNATGN\RWCSWSLSQARLLTSFL PAQL\RLRYQ\MLFTL\PGTPVFQAT GNEVIGLCSCPLLGPMPGGSQFML WDEVPAFP\DPGGC*VANMDCGR GQSE\DPGSL\LSL\RRLN\DQRSKE APPYCHG\DF\HAFLPLGPWTLSPH RQLGTQNETFSG*CLNLGDVGLSAG\ LQASDLP\ASAKPWPADKADLLSTQ PG\REEG\SPLELERLKLEPHE\GLLL RFPYAA
1041	6538	A	1088	652	905	HLLPPLTPTTTQWGRDLLSPISQM RKLRRHKVKKKTRT/WPGVVDHPL\ NLSTLGGGAWRIA*GQEFETSLGNI ARPCLYKKKFK
1042	6539	A	1089	3	591	
1043	6540	A	1090	266	1905	LGGHTWGTAAAGVWSDWPGRSW AELTSENSAGLSPSWGSPQDEVPGA WPMLQGAVEPMQIDVDPQEDPQN APDVNYVVENPSLDLEEFASYSGL MRIERLQFIADHCPTLRVEALKMA LSFVQRTFNVDMEYEEIH\RKLEAT RSSLRELQNA\DAIPESGVEPPAL\DTAVW*\VTRKKALLKL\EKLDTDLK NYKGNSIKESIRRGHDDL\G\DHYL\DCGDLNALK\CYF\RPRDYWTS AKH VINMCLN\VIKGRFTLQNW SHVLS YVSKAESTPEIAEQRGERSQTQAIL TKLKCAAGLAELAARKYKQAAKC LLLASFDHCDPELLSPSNV\AIYGG FCALVTF\DRQELQRNV\SSSSSFQV VLGSWEPQV\RDIIKFYESKYAS\C LRRLDEMKNLLLDMYLAPHVRTL YTQICN\RALIQYFSPYVSPDMHRM AAFAFNTTGGPPWKNELIKFIL\EGLI SARVD\SHSKIL\YARDV\DQRRITF* ESLCLMG\KEFQRRAKA\MMLRAA

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						VLRNQIHVSYPYPTQRKDARGELTPA NSQSRMSTNM
1044	6541	A	1094	2	397	SQDHVRGFLEKESAI\SRPLNPFTA KALSGTSPGDSDDVQPGPSVGPPSK DKDKVLPSFWIPSLTPEAKATKLEK PS/RLECVEKLIRKDMVDPVTGDKL TDRDIIVLQRRGGTGFGAGSGVKLQAE KSRPVMQA
1045	6542	B	1095	30	310	MTRHGKNCTAGAVYTYHEKKKDT AASGYGTQNI\RLSRDAVKDFDCCSL PRSCCHAYEKQ\RGTRREEQKELQR AASQDHVRGFLEKESAI*
1046	6543	A	1096	29	449	
1047	6544	A	1097	2	1069	IETRCTPRCRNSARGESLVRMTRHG R\N\CTAGAVYTYHEKKKDTAASGY GTQNI\RLSRDAVKDF\DCCCLSLQP CHDPVVTPDGYLYERE\AILEYIL\H QKK\EIARQMKGLTRKAGGGTRPPK EQKELQR\AASQ\DHVRGFL\EKESA IVSRPLNPFTAK\ALSGTSPGDSDDV \QPGPSVGPPSKDKDKVLPSFWIPFA TPRAKATK\LE\KPSRTVTCPHVKGS PLR\MSEPERPVHFHNR*NSS\VEPR GASITPQASAYVCA\VTR\DSLKRQ PPVAVLRPSGAVVTLE\CEVEKLIRKD MV\DPVTG\DKLTDRDIIVLASGAVT GFAGSGVK\LQAEKSRP\VMQALRC AGGPNKPGLGP
1048	6545	A	1098	5	576	SRVVEFAKMAENSGRAGKIIRDDSG VKGAVSHEQVIAGLQTTFGRNQRG LASQS\AAELGDWKLNEATALVIDT TGREV\DET\RKCYRMVWKEFLVEA NLSKEVACPAFGR\TTKEQIQKII*DT *HSSFQAKGKELK*ISGKKHNI/RVL MGEDEKPSQPKENS\EGGLGLKAS\S AGVVWSPRDQGLC\IFFLP
1049	6546	A	1099	534	1004	RMSAGALFIWGTAIYFDRKKTEVT PNFQEPGFRERRKKQKLAQGEKLG FPK\LPD\LKDAEAVQKFFL*RNTSL GEEL\LAQ\GEYEGK\VD\HLTKPELP VCGQPTASLLQVL\QQANFFPPPV\F QMLLD*SSPTISQRIV\SAQSLAE\DD VGMRNKCLH
1050	6547	A	1100	91	942	GLLVGVGAAAVMPGIVELPTLEEL KVDEVKISSAVLKAA\AHHYGA\QC DKP\NKE\FMLCRWEEKDP\RRCLE\ EGKLVNK\CALDFFKA**NRHCAE/P LFLQEYWGLCIDYTRPSKLFSTVR KQAGKSFDEC\VL\DKL\GWVVRP*PG ENCQKV\T\KVKTDRPLPENPYH\SRP RPDPSP\EIRGEILQP\ATHGSRFYFW TKLKMGPVAHTRSCAQTTT\DENAH AGLHPTDSGVLSGIHQHLTKKLT\YD DLAVILYHFLSIKIFKGEAPPLQHYF QSHQTTLCSPQNPNG
1051	6548	A	1101	140	812	GDFGDRAGAGRETEEIFHSSQQLKI RPWAGAGRAAEPKDWRIWGTGEW GSRQIPSPPVPSRSNPHFLPQAGAG

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						HFVQNPCKYPTPSPLQRSLEELPLSP TVFKLLHPDPPPCAPLTLQPVAPK *I*ESPPLPMLDPRDFPSPAPHPANE LKKRRGNPRQWFFLSEPRLSHLQN GTGWGWKGKDGRGRRTGMELGLI PEAPVPISGPPFIHSHSQPPCYTGL
1052	6549	A	1102	228	860	STAQGNLLTVFIQPRASMSGKY\V DSEGHLYTVPIREQG\NIYKPNKA MADELSE\KQVYDAHTKEIDLVP RPLNIFNG*PWSKIDFKDVIAPEGT HRF*RAFGKASFHLSL*KRYWFLP LCWSALFGHPRWALIWHGFTSANS LLFLAHL/WAVVP\CIK\SFLI*GFQCI SR/VSYSILRSTTGLVTPLFEAVG\KI FQQLSASNLQKEI
1053	6550	A	1103	825	920	
1054	6551	A	1104	222	1244	RWEKKMALLCYNRGCGQRFDPET NSDDACTYHPGVVPVFDALKGWSC CKRRTTDFSDFLSIGGCTKGRHNSE KA\PEPVKPEVKTT\GTKELCELKPK FQEHIISSPLSQ*KQLKRPSDPEMT NLGIKNIWPLKQALDKLKLSSGNE ENKKEEDNDEIKIGTSCKNGGCSKT YQGLSLEEVVCYHSGVPIFHEGMK YWSCCRRKTSDFNTFL\AQEGCTKG KHMWTKKDAGKKVVP\CRHDLHQT GGEVTISVYAKNSLPELSRVEANST LLNVHIVFEGEKEFDQNVKLWGI DVKRSYVTMTATKIEITMRKAEP QWASLELPAKKQEKQKDDTTD
1055	6552	A	1105	87	313	ISQERG*RRDKERLAQREIK/RRRER EK/ER*EERIDKKREAKREKR/ERER KIPEEREEERKKGIFVFIWFNPMSVP H
1056	6553	A	1106	37	404	PQLSRCRSECMYVNPTVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPVPCALGRGGRER WAAASFLYAPDPRPAH\VEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1057	6554	A	1107	19	919	AVWWNSELFLAGRRVLVTGAGK/G WAAGKGGQRPAAAGRGGQTPSLSP LPAGIGRGTVQALHATGARVVA\VS RTQADLDSL\RECPGIEPVCVDLGD WEATERALGSVGP\VDLLVNNAAV ALL\QPFL\EVTKFAF\DRVCPASRS FE\VNLR\AVIQVSQIVARGF/I*ARGV PGAIR/VNVSSQCSQRAV\TNHVSYL LPTKGVPLDMLDQG*WAL\ELGPH KLSRCRSELNASKP/TTVGD*RSMG PGPPWSDPHK\AKIMLNRIPLGKF EVEHVVN\ILFLLSDRSGMTTGS\T LPVEGGFWAC
1058	6555	B	1111	28	384	MKAAVLT\LA\VLFTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK

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						*
1059	6556	A	1112	44	1009	GGIREGGPPRPFRMKA AVLTLAVLF LTGSQA\RHFVWQGG*SPPRAAWDR V\K\DLATRVPTVTLKEQRTETYVS QFEGRLRGENS*TLKLL\DNWGQR* PSTFQPSCAKQLGP\LTQEFWYNLE KETEGFRQEMSKDL\EEVKAKVQP/ YTLDDFQERSWQEE\MEL YRQKV E PLARKNFQEG\ARPESLHELARRSLS PLGEAVSRPRARPMWDALRT\HLAP YSDEMMPALGRAPL GALRENGGAR MGQYHA\QATEHLSTLSEKAKPALE D\LRQGLLPVLESFKVSFLSALEEYT KKLNTQLRRPPPPYPVLRINVSKV EKKKKK
1060	6557	A	1113	62	393	IPAKQPTPTSLKTPTEECDQHENTAS SPSPMTTPCT/PSTNQPSKLPVSHSP NP*KPPAPKLLREMDLTFPPHFPPSV APTMKPLSSATTPMPRRISLSGSHSR RWDPFVG
1061	6558	A	1114	3	450	QTQREPTMVLSPADKTNVKA AWG KVG AHAGEYGAEALER\MFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNVAHVDDMPNALSALSDLH AHKLRVDPVNFKLLSHCLLVTLAA HLP AEFTP AVHASL DKFLASVSTVL TSKYR
1062	6559	A	1115	9	675	NSARATDSERTHGHARLLPDKTNV KA\AWGKVG AHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHG\SAQG* RAHGK\KVA\DALTNVAHVDDMPNALSALSDLH PQTALSALSGPATAHKL\RVD PVQL SSS*SHLPCWWTLGRPTSPSEFNPW RLHAFPGTKFPGLLVEAPLLEPSKLP LKLGLSLRVGHAFAPLGLPPRALLP FPGTRNPVGLLNKILNWGGKKKKK KKIF
1063	6560	B	1116	61	348	ESALTQLLKAGGSLKKFLFHPGDTV PSTARIGYEQLALGVIAAGAGAI VH EKHPGKLAGYISSLLTLGAFATAMA AVVLCVNSFIWQTEPFYIDT*
1064	6561	A	1117	2	256	CLS CAFWAGSVVIAAGAGAI VHEK HPGKLAGYISSLLTLTGAFATAMA AV VLCVNSFIWQTEPFYIDTVCDRSD PVFPTTAIVL
1065	6562	A	1118	3	270	AVVLCVNSFIWQTEPFYIDTVCDR S/DALFLAVCVLKVIVSLVSLGVGL RNLCGQSSQPLNEEGSEKRLLGENS VPPSPSREQTSTAIVL
1066	6563	A	1119	1	642	
1067	6564	A	1120	46	998	AIVPSWDLDDKDTISLLSPVLCIFPSPS SQTSLLYVFSLAGRMTQNTVIVNGV AMASRPTQPTHVNVHIHQESALTQL LKAG\GSLKKFLFHPGDTV PSTARIG YEQLAL\GVTQIFAGALRGVIL\GVC *SWGPGTVLRASGCAFWAGSVVIA AGAGAI VHEKHPGKLAG\YISSLLTL

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						A\GFATAMAAVVLCVNSFIWQTEPF LYIDTVCDRSDPVFPTTGYRWDAA KSRRNQWQKEECRAYM\QMLRKLF \TAIRALFLAVCVLKVIVSLVSLGVG LRNLCGQSSQPLNE/EKGSEKRLLG ENS\VPSPSREQTSTAIVL
1068	6565	A	1121	504	1026	KIKRKKKRPHIPV\LEIPGLLNIPCL WHLEWVTLSPSKRFAFAVGGN GGESGWLGGTRP/PSPRGMHLPSS SSESEPHRNCPCPGSAQPCGHQAGS EDPQNTGPVAS/EL*PPACWRLCGQ PGPL\GAPAAPLAGHPRPPWRQVGP GTSGSSQSWSSCDHGGQHSGQHQS SWQ
1069	6566	A	1122	461	548	KNLEQKNAMIHSAGEHHQGAERRS TWEELEGPRVTSLLV*RAWSSGP APSPT*PPSCTPPRRSS*APAGPSDAS PSRRPRA/SPASRQAAPKDKLPETPR RRIEKEP\PGPFAPGIFE/GGFTVSGG REQETPFAAGTSGCY/RTPPHFCWL GSPPRSTSSKAGGPSSSPSPTEAES STARPAKSRTMPTSGWHIGSTRPPR RRPSPR*RTSCTAHRRTSCSFGTMP ARSRGLHSEIRRLQQHCTDLTYELT VKCSEQTGDGTSKSSSELKKRCEELE AQLKVKENENAELLKELGAEKRDD SQCWRTPSRSRREKKYLGA
1070	6567	A	1123	148	197	DPLGFL*QKRNNQEDD
1071	6568	A	1124	1333	2383	RMKKEHVLHCQFSAWYPFFRGVTI KSVILPLPQNVKDYLLDDGTLVVSG RDDPPTHSPQSDDEAEIQQWSDDE NT\ATLT\APEFP*SLPLKVQGSYQIP LGGQVSFPKV*FGSAPRDIA YWIA MNSSLKCKTSLSDIFLLFKSSDFITRD FTQPFHCTDDSPDP\CIEYELVLEK WCEMIPGG\EFRCFVKENKLIGISQR DYTQYYDHISKQK\EEIRRCIQDFFK\ KHIPVQIL*MKDLVFDIYRDSRG\K VWLIDFNPFGVETDSSLFTWHEELIS ENNFKRRFLVKVDAQEQDSPSFSVA QTSEVTVQPQLICSYRLPKDFVDL S\TGEDAHKLIDFLKLKRNQPEGR
1072	6569	A	1125	162	413	GADGQINQQTLD DRS GDECLDECP GPPRRGKGPPQREVQPASPPGT HQ*GSDGSSCTSPV\SIGSPGLGPPI WRPHPKPG
1073	6570	A	1126	2	228	GGPRNKEPYPQGPKNRAQSPKNLV HSLTSM*SSP/LPFKPSKSTIHDNCPLT HQ*NPLKP*PLFPPSPNIPPGFKKP
1074	6571	A	1127	302	488	SPICLTPKSSLTHSSDDYKYSVWQR AVAHTCNPSTLGAEAG/WVT*AEEF KTSLHNIVRPCLY
1075	6572	A	1128	66	703	RRRRLPSVAIMILPGPSSSHDEMFS DIYK\IRGDRGRGLCLEGGRRWVS RTE\GTID\SLIGGNA\SAESPRGAK GTERHK*STGV\DIVMNHHLPGNKF SQKEASKKVHQRTMKSK\KGKP*K NRRPRKSKTFL*QGAAEQIKHILAN

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						FKKLQF/YFIGENMNPRWAWVLLL DY*RDGVPP\YMIFFK\DG\LEMEK MLTNVAIILDLSPOCH
1076	6573	A	1129	1	1006	LLLLGHASTSTGGGGKRASKMATT KRVLYVGGLAEEVDDKVLHAAFIP\ WGDITDI\QIPLDYETGEK\HRGFAF VEFELAEDAAAAIDNMNESELFGRIT IRVNLAKPMR\KEGSL\RPACSDND WLKKF\SGKTL*ED*RGRVRASQS RDPG/TGRAHLLKRRRSNPQVY\WD IKIGNKPAG\RIQMLLRSDVVPMTAE NFRCLCTHEKGFGFKGSSFHRIIPQF MCQG\GDFTNHNG/TLGGKSIYGEE VSMENFILKAYGDQGLLS/MLAC GDPNTNGSQF\FLTC*KTDWLGWA SHVVFGEVHRKALGCLCGQIEAQQ SKDGKPKQKVIIAGLWGSTC
1077	6574	A	1130	1	574	DTRFLERLRLSISFLVQTPIGHSTEED QGLLSTSLWGK\VKCGKNAGRKKP LGKAPLVVLPWPDPKRFL*KSGGQT LSLCPLPHPWGKPPKSQRHHGKER LTFPWGDAHKAPLDDPQRAFFAQA *VNLH\CDKPAMWDPENFQAPGEM LLVTVL\AIPFSGKEFHWPRLQGFLG RKMGDLELASALVPSRYH
1078	6575	A	1131	200	740	HGSMRRLLIPLALWLG\AVGVGVVSQ I*ENSPGGLQVALEEFHKHPVPVQW AFQH/TAVLESAVDTPFP\AGIFVRL E\FKLQQ\TSCPEEGTWKKPRVQKSR PQWDGNRKLPWPCIQTWALEDKSS WARLVPPPIKTQVLAGGWRSTQE DPSCLRVQRAC*RTPPSFYFPGQFAF SK\ALPRS
1079	6576	A	1132	79	933	EWSSIDLVLNELQVGISEKVSFLNR KIKPQVPLWYRLDGKVIILTAQAQ IGQAAALAFAREGAKVIATDINESK LQELEKYPGYSK/PRVLDVTKKKQI *SSLPMKLRDFDVLFNVAGFCPSRE LVLGL*GRKDWGLLR*ISMWRSTY LMDSRAFLPKML/RFRNLGNIINMS CCGLPSVKGVVEQDVCTAQPASR GLASTKSVGCRFHSRQGHSGANLC VARGTVDTPISYKKEYNATRS*TT ARE*FP*RDKKPGKIPQLPEEISHAL RRISASD\ESAYVTW
1080	6577	A	1133	1601	1778	MEQIRASGKLYKSLEYQKREIYIYMC STTYIYT*Y/HSTAYIYICLYVHIYIY MYRQYYVF
1081	6578	C	1134	58	394	MAEKPKLHYSNIRGRMESIRWLLA AAGVEFEKFIKSAEDLDKLRNDGY LMXQQVPMVEIDGMKLVQTRAILN YIASKYNLYGKXLKGESPFNLREQD AKXCLDPRGNPKIX*
1082	6579	A	1135	133	985	RNLRGIAILAGKPQVQFFHSRG\RM ESTRWLLAAAGVEFEKFMK/SLA EDLDKFR\NDGYFDVSSKCPMV*DL MGLKL\VQTRAILNLHLPANYNL/H YGGKDIKGREPLI*YCILGRY*PDFG

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						VEIV/LLSCLPYCSTLREQDCQALPW IKEKN*KNRPTFPCPLEKVLKRAHG TKTY\LVGKKS*ARAGPFHLVELSS TTVEELDFQSLSPSFPLPERPLETPES RQPCPHSERKFPYSPGQPQGKPSPW DEE/SL*EGRQKGDFSGFLINGSPWE GPRNLAINPMVS
1083	6580	B	1140	866	942	MDRHCPKLSGAPFGPPAPILGLTDP EFSHEPKLHHARILHRAPPPTRDHP VGVISRLPRAGRGRAGESPDPDLF*
1084	6581	A	1141	405	536	KSAPRPGVVAHTCNPSLGRG/G WIT*GQEFENSLANIVKCCFY
1085	6582	A	1142	49	365	TPDKPIRSHETLPIHEK*PRGKTGPPP DSDDPPPGSPSPQHVGNSSQKINSKLP ISSGDHSPNPYHW*CPLPSVLGIP/PV RRDPLCGPESPQEEGGQQRNESFDIF
1086	6583	A	1143	3	452	
1087	6584	A	1144	9	486	NSARATDSERTHHGACLLPDKTNV KA\AWGKVGGAHAGEYGAEALERM FLSFPTTK\TYFPHFDL\SHG\SAQG* RAHGK\KVA\DALTKRRGATWDDM /PQTALSALSDLH\AHKL\RVGPGSTF KLL\SQLPCLGEPWAAHLPA\EFQPL AVARLPWNKVSWGFC
1088	6585	A	1145	1890	2027	KCLCPPR/RCPQLTPYPC*GVKCPP SEIKYKP*MCPIGCPKPSIQC
1089	6586	A	1146	1	903	
1090	6587	A	1147	1	1131	
1091	6588	A	1148	1	1376	WALPAGFDGVMSHRKFSAPRHGSL GFLPRKRSSRHGKVKSPKDDPSK PVHLTAFLGYTPCL\AHIVREVDRPG SKVKNKEVVEAVTIVETPPMVVVG VGYVETPRGLRTFKTVFAEHISDEC KRRFYKNWHKSKKKSFTKYCKKW QDEDGKKQLEKDFSSMKKYCQVIR VIAHTQMRLPLRQKK\AHLMEIQ V\N\GGTCARES\WDPREGLKQQ VPV\NQVF\GQDENDRTSSGVTQGP KGLQRGSPSR\WHTQESCPKDPPE GLRK\VACIGAMAIPARVALPLWQR AGQEKATHH\RTINKIL*DLAQQ Y\LIKGGKL/VSKNNASH*PMTLSK S\NPLGGFVH\YGK*TNDFVTFKSL VWLGPKKRVLTLRK\SLLVQTKAA GLWRRITLKF\IDTTSKFHGRFQTM EEKKAFMGPLKKDRIAKEERSLMP GTDFAWWGLNKSYPFLKKKKK
1092	6589	A	1149	3	497	PTLLVPTDSERTHPWLLSPADK\TN VKA\AWG\KVGGAHAGEYGAEALER MFLSFPTTKTYFPHFDL\SHG\SAQV *GPRARKVADAL\TNVAQRGTIDIA QRACPLSDLH\AHKL\RVGPGSTFK LLKATC/HCLGEPWAAHLPA\EFQPL AVARLPWGQSFLGFLKQRC
1093	6590	A	1150	26	508	NSTDSETHPWLLSPADKDQRRGP AWG\KVGGAHVSRMCAEALERM LSFPTTKTYFPHFDL\SHG\SAQV*GP

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						RARKVADAL\TNAVAQRGTDIAQR AVPPLSDLHAHKL\RVGPGSTSKLL KPLACLVDPGPPTSPAEFHPLRLQG FPGDKFPGLSVGKFKI
1094	6591	A	1151	3	520	AKKHGHRGSSLTVFGGPHRLRENPP WCSSPADKTNV\KAAWGVGAHA VRSMCAEALER\MFLSFPTTKTYFP HFDLSHGFCPG*RATAKKVA\DAL KRRGATWDDMPQTALSGPEATLH AHKAFGVPGSTLKL\SHLPCW*P LARPPSPAEDPWRVERLPWDKFP WVSC
1095	6592	A	1152	232	783	TCNPQTSSNGSQNSKLGRISRKWR MRRFCFSITRWLECTSPRSRGRW KTDDVLLKLENMGVSELGQRI*LER FTKDTARFKDELDIMKFICKDFWTT VFKKQIDNLR TNHQGIYVLQGNKF RLLTQMSAGKQYLEHAS*V/Y*HLP CGLIRGGLSNLG\IKSIVTAEVSSMP ACKFQVMIQKL
1096	6593	B	1153	28	249	MFLSFPTTKTYFPHFDLSHGSAARLR ATARRWRRADQRRGHVDDMPNAL SALSDDLHAHKL RVDPVNFKLLSHCL L*
1097	6594	A	1154	3	511	DKTNVKAAWGVGAHPGEVWCGP LERMFLSFPTTKTYFPHFDLSHGSA QVKGHGK NVADAL TNAV/AHVDD MPNALSALSDDLHAHKL RVDPVNFK LLSHCLLVTLAAHLPAEFTPAVARP SLGQVSWAFL*SNRCWTFQISLPAE FTP AVHASL DKFLASVSTVLTSKYG
1098	6595	A	1155	2	247	PADKTNVKAAWGVGAH/AGEYG AE/ALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGK KVADAL TQGELGG EVGGQGHQQA VA
1099	6596	B	1156	74	195	MFLSFPTTKTYFPHFDLSHGSAQVK GHGKKVADAL TNAVXT*
1100	6597	A	1157	3	224	
1101	6598	A	1158	3	136	
1102	6599	A	1159	1	371	TQREPTMVLSPADKTNVKAA/WGM FLSFPTTKTYFPHFDLSHGSAQVKG HGKKVADAL TNAVASVDDMPNAL SALSDDLHAHKL RVDPVNFKLLSHCL LVTLAAHLPAEFTLAVHAFLGQFP GFF
1103	6600	C	1160	1	156	MVRRPWRCSCSPPGXPPRRRVHP CGAXLPGQVSXFCEQRAELQIXLRL EL*
1104	6601	A	1161	1	577	AAWGVGAHAGEYGAEALERMFL SFPTTKTYFPHFDLSHGSAQVKGHG KKVADAL TNAV AHVDDMPNALS LSDLHAHKL RVDPVNFKPPRPTSRT ST*ATALPRLRATARRWPTR*PTPW PRGRHAQRAVRPERPARAQASGGP GQLQ\LLSHCLLVTLAAHLPAEFTP AVHASL DKFLASVSTVLTSKYR
1105	6602	A	1162	1	680	ERTTMVLSPADKTNVKAAWGVG

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						AHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGGRGMMVAQVAHQVDDMPNALSALSDLHAHKLKRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLT SKYR
1106	6603	A	1163	2	1758	TMVLSP/ADKT/NVKAAGWGVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKL/RSRTST*ATALPQVKGYGQEGRRVDQRRGARGRHAQRAVRPERPALR NKLWVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLT SKYR
1107	6604	A	1164	121	521	SFNKFFKKAKAVSQKKIPATKLRDKGLQTKYSCLYYYFYLRHGLALSPRLACSGTITAHCILKHRGSSDPP*T*ASHVLKLQYFCTS**LGITGACHHASLLLKFFVETDLTVLPRLVSNFWPSSCPSL LKCWD
1108	6605	A	1165	407	548	VPFTKWHQKIEAGQAWWLMVPVPAVWEAEVAGGSLEIRSS*PAWATW
1109	6606	A	1166	25	628	EFHRLRENPPWCLSPADKTNVK/APAWGKVGHAHAGEYGSEALER/MVLFPPPTPKPYFPHFDLSHG\SAQV*GPRARKVADAL\TNVAQRGTDIAQRAVPPLSDLH\AHKL RVGPGSTFKLLKATC/HCLGEPWAAHLPAEFQPLAVATSSLGTFKFPGLVEAPLLTFQITFKGWKLWLAIVFLPFGLPSPSPFLHPYPRGL
1110	6607	A	1167	2	121	TFVRLGTLSTPLWGSYDFFFPS*FSLFLFYSVHFMPPLAF
1111	6608	A	1168	3	582	AKRELRFLLVYLHGDDHQDSDEFRCR\SQLRENTYPFLAMIMLKDRRMTVVGRLEGLIQPDDLINQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLRADQEKERKKREERERKRRKEEEVQQQLAEERRRQNLQEEKERKLECLPPEPSPDDPESVKIIFKL PNDNRVERRFHFSQSLTVRTT
1112	6609	A	1169	30	130	QILLSPCLPPP*YLNKRWPEDNTCLLKTCLKRT
1113	6610	A	1170	2	1412	GIAGPTISCRGGGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNWNIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSRLPQPRGLLGWGYLIMLPFRFTYITI LDIFARFAPRFIR/PEP/RSR/VT*PRLGTIVSIYGTPEEKYGRAHPVFYQGTYSQALNDAKRELRFLLVYLHGDDHQDSDEFRCRNTLCAPEVISLINTRMLFWACSTNKPEGYRVSQALRENTYPLAMIMLKDRRE*PV/VGRLEGLIQPDDLINQLTFIMDANQTYLGV/SERLEREERNQTQVLRQQQDEAYLASLR

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						ADQEKERKKREERERKRRKEEEVQ\ QQKLAEEERRRQ\NLQ\EEKERKLEC LPP\EPSPDDP*KVSKIIF\KLPNDSRV ERRIPLFHRSLTVIHDFL\SLKESPEK FQIEANFPRRVLPICIPSEE\WPNPPTL QE\AGLSHTEVLFVQDLTDE
1114	6611	A	1171	232	427	STKISHTKKKTARINKTKGGRGQAW WLSPIIPTLWEIKVGGLFEPRRSRLQ *AVFMP\CTPSWATQ
1115	6612	A	1172	232	427	STSISHTKKKTARINKTKGGRGQAW WLSPIIPTLWEIKVGGLFEPRRSRLQ *AVFMP\CTPSWATQ
1116	6613	A	1173	77	1775	GRKVVMIDLIPNLAVETWLLAVSL\ VLLYLYGTRTHGLFKKLGIAGGTPL PFLVNALYFRKGYWTFDMECYKK YRKVWGIYDC*QPMLAITDPDMIK TVLVKECYSVFTNR\RPFGP\VGFMK NAISIAEDEEWKRIRSLSPFTT\SGK LQGDGPLSLPQYGDV\LRNLRREA \ETGKPVT\KDVFGAYSMDVITSSSF GVSIDSLNNPQDPFVGKHQGSF*GF NPLDPFVLLQLKVFPFLTPILEGIKY SLCFPRKSY*VFLNKIC*NRLKEGRL KETQKHRV\DFLQLMIDSHKNSKDS ET\HKALSDLELMAQSIIFIFAGYETT SSVLSFIIYELATHPDVQQKEQNEID T\LPNK\APPTYDTVLQLEYLDMVV NETLKLFPVAMRLERVCKKDV\EIN GMFIPKGVGV\MPISYVLHHD\PKYW REPEKFLPERFSKKNKD\NIDPYIYTP FGSGPRNCIGMR\FALMNMKLALIR VLQNF\SKPKETQIPLEI\DAVGGL LLTEKPIVLKAESRDET\VSGSLNFPK DILVCSLRKLVPQKHQRPSNYFTNR PLKRRRGFIPNVAAIK
1117	6614	A	1174	3	403	
1118	6615	A	1175	2	465	
1119	6616	A	1176	1	1112	AGEFPGQLHSRAS\FC\TARSGSAAAL RMRPVRLMKV\FVTRKIPRPRC\VA LARAADCEVEQWDSDEPIPAKELER \GVAGAHGL\CLLSDHVDKRILDA AGANLK\VISTMSV\GIDHLALDEIK\ KRGIRVGYTPRLSLT\DTTAE\AVS\ LFLPT\CGRWPEAF\REVKNNGWTS WKPLWLCGYGLTQSTVGII\GLGPH* AQAIARRLKPF\GVQRFLYTGRQ\PR PEEAA\EF\QAEFVSTPEAGWPNLILI VVACSLTPAT\EG\CKK\DF\QKMKE TAVFINISRGD\VVNQGRPCTRALAS GK\IAAAGTGM*T\SPELPYKPPFSL TLERIVVILPHIG\SATPQEPGNTMFL VWAVNNLLDGLRGE\MPSELKL
1120	6617	A	1177	518	780	EVLPSGPGLLALVLR\LGSEFKLPHH EVSVGT/HPCQTSGAPARHRSTRDP VFPLSRGHNNPVPSWKHRAALTRH QTFLYCERGLPACIH
1121	6618	A	1178	117	1166	ITMATGQKLMRAVRV\FKFGGPEVL KLRSDIAVPIPKDHQVLIK\HACG\V

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						NPVETYIRSGTYSRKPLLPYTPG\SD VA\GVI*A\VGDNASAFKKGDRVFT RQARSSGG/YMAEYGFFAGRTTLFY KLPGKTGTFKQGSLSDFPYFYCFIR GL\IHS\ACV\KAGESVLVHGASGGV GLAACQIA\RAYGLEVLGTAGTEEG \QKICFCKNGAHEV\FNHREVNYIDK IKKYVGE\KGIDINEMLANVNLSK DL\SLLSHG\GRVIVV\GSRGTIEINPR DTMGQRSPSIIGVTLFSSAKEVEFQQ YAAAL\QAGMGIGWGGPVIRSQYPL ERVAEAHEDIHGS\GATGKMDSSL MDD
1122	6619	A	1179	264	647	NLGTCPFPVPALQCLLVETVSRGS LLPVSPLLFQLLYPSPPA\PSYSINSL LPP*PCPASLPFYDSL\YI*RPAPF*SH PSPSTPRTEGGV\PSQSHPPCCPQAP APPPSLPASLSQRHLLPPLSHHSC
1123	6620	A	1180	1	575	NFALEAKNSARAISVVQTPIGHSTE EDQGLLSTSLWGK\VKCGKNAGRK KPLGKAPLVVL/HPWDPKGSFEQAL GNPVPPALCPSWGNPPKSRAHGK\K VLT\SLGEMPIKHPG*SSKGTFAQPD VNCTCDK\LVHDPENFKLLG\NVLV TVLGNPIFGKEFTPEGCRASWAERW VTWSWPVPCSSRIPLKPLGP
1124	6621	A	1182	265	714	HFTYKYTAGTTIKSKNICITPKSYSC TFLVINTLTTPLSNHYSGFSLRLVLI VLEFFLFWRWSLALSPRLECSGMIS AHCNLCLLD*SDSPASASQV\AGITG TRHQACLIFVFLVETGYPHVG*ARL ELLTSGDPSPWPVKVLGLQT
1125	6622	A	1183	84	1009	HSMMMkipWGSIPVLMLLLLGLID ISQAQLSCTGPPAIPGIPGTPGPD GQPGDPRG*KERKGFQGLAGDHGE F\GEKGRPRGFLGN\PGKKFGPKG\P MGPKVGPGAPGTPQAPKGDSDYK ATQKIAFSATRTINVP/LLRRSQ\IRF GPR*FTNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVSRG\NLCVN\LMRG RERAQ\KV\VTFC\DYCLTNTFPGPPP VGMGPQLKKAPKGGGGGEKKTV\F LQA\TDKN\SLTGAWEGA\NSIFSRV PGFFPDMGGPDLWAGFTSTPGSPCP ATLTIPPTTTI
1126	6623	A	1184	115	361	GWRGLPHCVPGRNCCSVLLMGs/C CL*GPHAL*KPSCSVRCWPEAPLH SKTDPRLSAA*PPFC*VR*MRYGLR TVCAQILSV
1127	6624	A	1185	3	734	GGSRERARPSERRLPSRRSAPHRP PPQPCEQDNSPRKIQFTVPLLEPHLD PEAAEQ\RRRRPH\ATLVLTSD\QS SP\ETAEDRIPNPHLKSTL\AMSPRQR KKMTRITPTMKELQMMVEHSPGGN RQQGEEP*RGPLESTG\LQES\RPPGI PDTEVECKCWAPFGTAKK\TAECIP\ KTHERGSKPESTKEPSTH\IPPL\DSK GANCGSERGGGILGSRLQFGNAWT

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						PDLFLIPSLLGKISCF
1128	6625	A	1186	1	1359	GGPRDVNCRCLRLRAAETPPAWHL CMRSGAPTPPAAAMESETEPEPVT LVKSPNHRHRDLELSG\DRGWSVG HLKAHLRSV\YPERPHPEDQRLIYSG KLLLDHQCLRDLLPKQEKRHV\LHL VCNVKSP/SQKLPEINAKVA*IPQRE PVGSN\RGQY\PEDSSSDGFKGKGKF FR\NLSFPWGW\ENIFKGLEACPSRH FQGLG\PGFLPVYTPYGV\WLQLSW FQQIYARQYYMQYLAATAASGAFV PPPSAQEIPVVSAPAPAPI\HNQFPA\ ENQPANSGMLAPSSGLFNP\G\ANQN FAG*IAQGGPIVEEDDEIN\RDWLD WTYSAATFSVFLSILYFYSSLSRFLM VMGATVVMYLHHVG\WFPFRPRPV PNFPNDC\PPPDVVNSDPH\NN\LRE GTD\PELKDP\NHLPP\DRDVTRMGE AGPGPFLYGGTAWVCSFKDFSLASS FFPEGPPSPSAN
1129	6626	A	1187	314	1614	
1130	6627	A	1188	128	1910	RVVDRGRRWDSPLGGLGTWPGR SSLRFASASSDSDSLGLYRASLHPS PGRAALGLCLYLTKTSCCAAIGTLY WGNIAWKQEAYSLSGENFFMSETE NSCSPFMSSLLQTEDTKKLQSKNL FILLIKPTNPKMSVNVNPQRCQTQ FYRLQDAPRLIAQG*GAKGNGNPR PVI/MSNMVDVGKGLIGPPNVSPPN IPIELGAQTQFDVKNDRIYVNG\SH GGELSCQDMLADGFH*KNFVLC\PEC GGFLETDLH\VNPK\KQTIGNS/CGK ACG\YRGMLDTHHKLCTFILKNPPE NSDSGTGKKEKEKKNRKGKDKEN GSVSSSETPPPPPPNEINPPPHTEEE EEDDDWGEDTTEEAQRRRMDEISD HAKVLTLSDDLERTIEERVNTLFFLF LNKIKEEGVIDSSDKEIVAEERLDV KAMGPLVLTEVLFNEKIREQ\KKY RRHFLRFCHNNKKAQRYLLHGLEC VVAMHQA\QLISK\PHILKEMYDAD LLEEGFFISWSEKASKKYVSKELAK EIRVKAEPFIKWLKEAEEESSGEEEE DEDENIEVVYSKAASVPNV\EFVKS DNKDDDD\IDIDAHLLKGWMQPSLTV
1131	6628	A	1189	132	362	RRVDWKIQKISIGSS*KLFNESHGI FLGLQRIDEELTGKSRKSQLVRSK NYRSVIRACMEEMHQVAIAAKDPA NGRQFSSQVSILSAMELIWNLCILF IEVAPAGPL
1132	6629	A	1190	97	355	AFSYNCPSPKISCQRKSQHFHLGGLY VILFLFQKGQGVCCQSHPERPEGNP RRHQGQKERSCVGKTLL*LPEQDFV PEKVSAFPWWSLCHHPVSVPKGA RRLSAESSRKTTGGQSETSSRTEGEK LRRQNASPRTYGGTRDTFPGMSVG H
1133	6630	A	1191	137	474	

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1134	6631	A	1192	307	583	
1135	6632	B	1193	1	969	MRPYSQTVFSTQYRWVEQHLGPQF VERIILTRDKTVVLGDLIDDKDTV RGVHKSMCPGVTAASWGRAKDAM SICGCWLRELWDTSSRENSAAVKT GREADKPEVTKQTQFSTRKDEQAC SGYPYSDCWLAIELLHSAEPQAPRS RSDANASRSGPLRAGCETRLRLGV SCSACKPKPSVLRCLLSARPLCGP LHASFLPGVDSKSGKTAPRTDCTQS TALTGSGGAGDTLRIDEELTGKSRK SHTQVFICTSPLLKYHHCVGEKYR WVEQHLGPQFVERIILTRDKTVVLG DLIDDKDTVIRGWTRYWPQSSLA CPD*
1136	6633	A	1194	834	1834	PSWCCRAGWMKPKDKMLSKEADAS PASAGICRDHGGPDEDNAHS*SWE HPDTRDAGAASGSTGTRNVERYLQ DSTFATSPHLAESLLKIMLGDEAALL EQKELLSNWHYHFLVTRLLYSNPTV KPIDLHYAQAQSSLDLFLG/E*EQPSN PWTWSCWQPLSLTS/NVIKECSIALS NWWFVAHLTDLLDHCKLLQSHNL YFGSNMREFLLLEYASGLFAHPSLW Q\VGVDYFDYCPELGRVSLGAAHLS GYL*TPRQKA\RKVLRICEAAADD* TSSQHL*DLSHESPSATIAWVLASF WSIRVKGCRLCPRSCQTGSSGITVSE AAFLIWISLATWGQP
1137	6634	A	1195	32	393	
1138	6635	A	1196	102	888	RNLQETAIMEAEP\KLHYFNARRRM ESTRWLL\AAAGVFEFEKFIKIWQ KIWDKFKEMMGYFDVVSQQVPN/VV *D*WGWLKVQTRAIQLTFASKLQP SYGGKDIKGRRALDLI/DVF*EGFSQ ILGLKLFPPFLPVMSPHEEKRCPSLA LGSKRKIKIGYLPPEKSLKEPMG QDYPCWANKLEPGLDIHL\VGTFY YVE\ELGLLGLISSFPLLEGPWKTRI QLTCPTVEEVSLQPRAPREAPPRD EKPLEEAKEDFPFG
1139	6636	A	1199	46	399	PGSKYDKTAILVSHLNFNLNLIKQP NPTQISPQGMFKRGGAR/PLLKTGPF LPTWGKDSFCYKHSNSGWFEAKG FRRLPSFKNERKRNIIGSPPPRLVVIS SESPHAPFGTKSIPED
1140	6637	A	1200	37	454	PGSKYDKTVILVSHLNFNLNLIKQP NPTQISPQGRPPPPQCRVTEWTTTAS TQTQAGLKLKDSDDFQVSRMKEKE T**GAHHQDL*LFPQKAPMPHL*QN PFLKTDSSRNQVRSRTFPTSITFQNV GRSLPNTIYSGKK
1141	6638	A	1201	298	523	LLKVQSRQKHVAVGLRTLVRGA VLIRVPPLREPLAPPILVGASSRENI SR*VTGCSPTHSSTPPLATSPRQRA
1142	6639	A	1202	80	589	IFLNLLIKQPNPTQISPQGRPPPHVQ GD*VYNYGPTPASQPERRALKRGI* RKGEGGPRERVWAGAPPGLPTPF

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						PENQGEKACG/GGRCLSPISSLQGPR FPADWWEIPIL*SPDLHRDWGPAPP PPTSSNRPTPTVLRQERSGLG\PPSP GHLGKLVFFQLAWDSFL
1143	6640	A	1203	2	661	FVEADRGLAVGSLRPLNLRGARA AFRFAAGRESRGKGTGERRTRVA VAGKVTSVPFVVSQGREHSHAPTR LPTIPPAAMSAAGVARGLRAA\YHRL LDKVE\MLPEKLRPLYNQSRQVPR TVFFWAPIMKWGVVCAGLA\DMA QTLPEKP*AQLQSACFGWLTRGLIW \SRILHL*IIPNTNWSLFGW*FPFVG AAGASQLF\RTWRYNPRTKKLKAH K
1144	6641	A	1204	20	400	
1145	6642	A	1205	457	1011	SRRPWGHFTEEDQGLLSQSLWGQ/V *NVEKMLGRKKPLGKAPLVVLPW TPRGSEKALGNLVLLPSCPSMGNP QKSRAPWARRVLTFPWGDAHKSTP G*SSKGTFCPA*SEPA/HCDKLH/VL DPENF\KLLG\NVLVTRFGQSIFGKE FHPLRCKAS\WQKMGEQVGHFPV LQIPLSSL\PMMQSFQG
1146	6643	A	1206	3	452	
1147	6644	A	1207	9	485	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGGAHAGEYGAEALERM FLSFPT\TKTYFPHFDLASHGFCPRK GPRQRRWPDALTKA\VA\HVDGHA QTALSGPEATLHGAQSGVDPVQLS SS*SHLPCWLTGRPPSPAEFNPCR V ARLPWNKFPWVSC
1148	6645	A	1208	37	298	RQGLPLSPRLECHDRIIAHCNLEVLG SSSPPTPASPIA*\TTGVGHHTQLPFK LPYFFHSGLFFFLKKILYQFCDTYRA RISSDFCR
1149	6646	A	1209	49	564	SQTPMGHFTEEDKATITSLWGK\W NVEK\SWKEKTPGKGSLVVLPWTP RGSF\DSFGQTCPSALCPSMGKPPKS RAPWPRRVLTSLGRCQQSTWDDPQ GAPFAQA*SELHC\DKPAMWDPE\N FKAPGEMLLVTRFGQFHFRANKFTP EGCRASWAERWVTGVASALVPSR YH
1150	6647	A	1210	134	673	QRRTKATITSLWGKGEMWKDAGG E\TPGKGSLVVYP\WTQ\RFDD\SFG\ NLSSAFCPMGKPPKSRHLHGK\KVL TSLGRCP*KHLDDLNHLLPKPDV NLHC\DKPAMWDPGGTFKLPGENV AGLTRFWAIPFSGKEF/TPLEVARLP WQKMAEDGDWQWASCPVPPRIPL EAHWPMISELFKG
1151	6648	C	1211	50	373	MGTVGSAWAAAPVQTHMFCSSSSC ISSLSTLPDAAAPLSPLASSWPVPPRP LLHWPFQDQSSLLFSLSPSFXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX RALHTSLA*
1152	6649	C	1212	45	424	MNGDXGLCLAAAPDQTHMLGSSSS

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						CISLSTLPDSPAAPLSPLASSWPVPP RPLLHWPFQSSLLFSLSPSFXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXLTHTFSLERGGVLSISIRMW VRLS*
1153	6650	A	1213	97	1382	SACAWRLPSPGPSAMWPLWRLVSL LALSQALPFEQRFWDFTLDDGPF MMNDEEASGADTSGVLDPDSVTPT YSAMCPFGCHCHLRVVQ/CAPTL GLKSPKEISPDTTLLDLQNNDISEL RKDDFKGLQHLYALVLVNNKISKI HEKAFSPRLKLQKLYISQNHLEIPP NLPSSLVELRIHDNRIRKVPKGVFS GLRNMNCIE\MGGNPLENSGFEPG\ AFDGLKLN/YT*RHLQRSKLTGHSP KYLPELNLHLDHNKIQGHRTGR DLLRYSKLYRLGLGHNVQIRMIENG\ SLSFLPTLRE\HL\DNKKLAR\VPSG FPDLKLLQVV/YILHSNNIHQSGVF NEFLFPWFGGGEAGPYNGHSASF TTPLPYW/ERLQPATFR/VVTDRLAI QFGQLQKVEAAAATLVSQWGS LG NRARHPDGEAEPGS
1154	6651	A	1214	938	1501	AGVGPDPGFLFQGIVANDSHPTALL KRMFASGGRRSWCQPFQGT PAMG GPWAKGCLGPASCAAKVGGPHPKT NPGPKPTGGQGFPATGLRGVGISPP K*PCQ*AVQPGSHCPATCAEPSPPW G/PGVPRFEAPPPQTPP*PRLWPETG EPPLGVQKPP/QPMPGPGAPLEN*S ASGGPRSPRGWESVWF
1155	6652	A	1215	883	1216	YISNSQLVQHFFFFFFFLFFETESC PVAQAGTQWCDLGSLOPPPPG*SN SPASASRVAGITGVHHHAGANFLYL *QRWGFTMLAQAGLELLTS*STRLG LPKCWGLQT
1156	6653	A	1216	197	821	RLFHSNQTVDSQKNVDITLKG\RP SNRVRA PKGTL\RD FNPHQM*NSA LLGKEQQRGFRVD\KWWGYQKGN WPTRSGLFGSHVQD\MIKGWLPGL PVT KMR\SVYAHFPHPTLLSRENGV SLLKSRNFLG\EKYIPQGFRMKTRVL LCQYLKAQKR*N*SLEGND\IGLVS\ NFSRLLIPASPTRLKTGKIRK\FLDGI FCLLEKGLFRQA
1157	6654	A	1217	241	514	DGQRLGKPHFVLLVLQ*LQTGLWS WWGKLG VGE/MLGVGEILGSAFISP VLERVEGSGSGGNQAGPREEGWLG KPLRPEAPPSTFIQHHTLG
1158	6655	A	1218	3	496	SSGLFTQQSPEAWFCVSKCSYP AW QNVKVIVDSHKLQEIIQSLIPFAQF PAMVTVC KAPGRFCHPCWHV*P/HP HSHDTEHGHHHKCLVLCYPFTASA PPSCPAPLR CIYGCILSCLVDVPWRT DRLNKQRVCKEAQSRREGSPA WLI GQHSRLALPLLAALS
1159	6656	A	1219	1326	2014	QLMIYTFRTELAHWPGDQKH YFHT CVMILFFLRQSLALLPRLGVQWHD L

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						GSLQPA\PPPPGFRLFSCLSLPSS*DY RHVPPAPQLIFFFVLLVETGF/TPMLG RMVSI*/PSDDPPTSASQSARITGVS HSWVNSCDLPLKNFFFFLEESHVS QAGVQWHDLSLQPPPLPGFKLFCL CLLNSWDYRHAPPCPANFCIFSRDG VSPCWPAWSPSLHLVIRPPWPPEVL GLQA
1160	6657	A	1222	1	459	IEIHIKCGGIPAVLAAPAMGLELFLD LVSQPSRAVYIFAKKNGIPLELRTV DLVKGQHKSEFLQINSLGKLPTLK DGDILTE/SANRSVYLQGGCWHIT EMRFSKCKAEGPAKSRSAIILYLS KYQTPDHWYPSDLQARARVHEYL GWHAD
1161	6658	A	1223	2	310	
1162	6659	A	1224	205	454	
1163	6660	A	1225	2	384	
1164	6661	A	1226	1	1276	MPGLGFREKKGGSRTVIPASRGCG PAPILCTKWELPLSGSSRCLAAAL QGTVWTAESSSLTPAFQSRGWGLIP YFPARRDPATAAAHTALSAFTAIPA VLAAPAMGLELFLDLVSQPSRAVY IFAKKNGIPLELRTVDLVKGQHKSK EFLQINSLGKLPTLKDGDFILTESLA LIYLSC\KYQTA\DHWP\SDLQGF ARVHEVPWAWHADLHPVGTFWY YPWGVQGVWGHSLGVQVPEEKVG TQTRTAMDQALQWLEDKFLGDRPF LAGQQVTLADLMALEGS*CKPVAL GYELFEGRPRL\AAWRR\RVEAFLG AELCQEAH\NIIISILEQAA\KKTLP PSP\EAQYQAMLLRNRPSPGSGM GAKEISNKDSFCYLLAPFYLSLLPQS LLSKLQCEALHRQRHSSVLWQVLL LLRCKHT
1165	6662	A	1227	151	278	G*KYDSDIYHEAVVPHQNQMSARS DKEKKRFIFYSSYYIPFC
1166	6663	B	1228	1	690	MASWDEKDLTVPQPDTRKGSVLRC GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGYELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
1167	6664	B	1229	1	975	MSPPGREQGLLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWWVDSADRQRMQDCQ RELQSLLEEVEGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLQL SSLTCIYTAGKMRLQDRIATFFPKG MMLTTAALMLFFLHLGIFIRDVHNF

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						CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH*
1168	6665	A	1230	1	211	
1169	6666	A	1231	950	1326	RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCLA CLPLRTECLGIKPIVHLFSCTRPVIV PSLELNVDVDSIAHMFVADLLMIT LPSYDIPFYCLVFQNLVLEFQYL
1170	6667	A	1232	271	927	NQGLRHVRLCRMCLVNQMFASSIL GKSHHSLVPINQGHNALWKAAG\ PLPLKAGYC\QGFSFCHSLKYG\SW DEKDLTVPQRDTHKRSVLKVELVQ RGKNLPVEDGGKAHCLPELPPGELE CPG\ILKHGLYHWSSSEMGEKPAPM VGG\RHV\CSNAALVPLLPLRCLGG EKHKSGL\HARPV\VPSELNHDTD SFAHMFADLLLIITLPS\YYIPFC
1171	6668	A	1233	62	1158	GHLCARPETSLLQVRGPPLPSSFSG MDVGPSSLPHLGLKLLLLLLLLPLR GQANTGCYGIPGMPGLPGAPG\KDG YDGLPGPKGEPG\PAISWIRGPKQG KGEPG\LPGHSWGKMGMMPGPGDC QGLPGPLGDFPG\EPG*G\GRYKQKF QFSFSLIRQTHQPPRT\NSLIRFNAV L\TNPT*IYNTCTG*FTSKVPGLY\YF VYHASHITANWCVVLYRSG\AKVV TFCGPHVPKPISSNSGGCACLRLOV GRGRCGWLS\MTYYGHGWGIQGL* KSVFSGLPWLLPRTKGGARCGSRPT GPSPSPQLPAWTQPYWPVCILALDH SPHQMDFSPPGSPPLTHPHCTPLPM GSLPLNFFRSHCLCGSWDT
1172	6669	A	1234	2	907	AVAFGAKGTDPAEARSSRGIEEAGP RAHGRAGREPERRRSRQRRGGLQ ARRSTLLKTCARARATAPGAMKM VAPWTRFYNSCCLCCHVRTGTILL GVWYLIINAVVLVDFIECPG*SGSSI TFQVLELGGDFEFMDAN\NGAFAI AISLLMILICAMATYGAYKQRAAWI IPFFCYQIFDFAL\TC*VAISGLIYANS IQENIRELPPKFPYRDDAMSVNP\TC LVFIILLFISISLTFKGYLISCVWNCY RYINGRNSA*CPWFMLPAMTLRCC YPPYDDATVNGAAKEPPPPYRVCLS L
1173	6670	A	1235	966	1564	NDFFKTNKSSIIRNSCLTAILVFLCC YDLTLTGTLF*ILTFRWL*LGLIIRLN \MASRSTIYVYGSQPSFLFTFENTDF YQLWILFLVICLPFLFKLFTIFLWP KLLTLENQILHQIQCFSVVFLMSAPI TTVRGIHVLPVIVILQTDLAWINQLL HLLFSKLGYYDDSVQDWVSLMWN GTHGRKCRSQFYMPIKHL
1174	6671	A	1236	155	303	AFQEGDPMFKPSRCPCPYLPKPCPS TCLP/SFAFRAVVTQVP*CCVCKCPG
1175	6672	A	1237	739	1629	GTSQMPTSAVPSLLSPSKFARKGFS

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						KVLQLCLYRRIGLCPAPPPPPVPTQC PRPQELIGP/WRE*CPPGSFRNSPRNL FSFLQELPEESV
1176	6673	A	1238	1	554	NFALEAKNSARAISSLVPDA\MGHF TEED\KAT\TSLWGKGEMWKDAGG ET\LGRL\LVVYP\WT\QRFFD\SFGN LSSASAHPWATPKVKAHG\KKVLT\ SLGDA\TKHL\DDLKG\TFCPSLK*TC TC*QACNVGS*GTFKLPGEILLVTRF WQSHFRQKNFTPEGCRLSWAERW VTWSWPVPLFLPDYH
1177	6674	A	1239	29	454	
1178	6675	A	1240	1	1368	
1179	6676	A	1241	1	1266	LSRVAEFEHLGWSPKPPTTCTPACQ GLSGAAMKSLVLLLCLAQLWGCHS APHGPGLIYRQPNCDDEPETEEAALV AIDYINQNLPGYKHTLNQID\EVK VWPQQPSGRAVLRFEIRTPWGTTLP CCWDPTLVGQDASLEGLSKEHAVE GDCDFQLKLDGKF\SVVYAKCD\S SQDSAEDV\RKVCQH\CPLLA\ND TRVVHAAKSCPGPPFNAQNNGFQF FSLEEISR\AQLVPLPPS\TYV\EFTVS G\TDLLFA*KKATEAAKCNLSGQKS NMGFCK\ATLSEKLGSGQRLQLTCT VF\QTQPV\T\SQPNPEGANEAVPTPV\ VDP\DAAPPSPPLGAPGLLPSWLT PKT TMVLL\AAPPQHQLHR\AHYDLCHT FMGVVS\LGSPFRRKCSHPRKNT/RT VVEA*WLGAAAGATGFLPLFRGGI RHFVK
1180	6677	A	1242	1134	1247	
1181	6678	A	1243	1330	1517	KLNMVFKKISHGMQLRKSYNLFYQ KSGKIMT*IWEIFFPEFFFIPTTY\LF LKREFLLNEPS
1182	6679	A	1244	213	287	
1183	6680	C	1245	249	323	MYKLRRKLEDRNKIENENIVKSFR*
1184	6681	A	1246	1021	1985	IAWAFKINWLPIIFLIFSVLFPYIFGFI FFYLLYFSNTCLS/FVFPFSYLKLLTI FSFSILFLSSNFLSLYLPLAFCFLAC LFFFCFLFRFKFIFFLPKSMFLSSNF PIF/CIFFFFAFPYSCLPVFHCQTFYLL QIVVIL/IHSQLIFPFSSAFSKCG*QGF *MTQFSLRHGFQGLLITFGLISF*KIA FKLF*SPTTFKLNFKLKF\YLHFNK ALPSLLGLNSGLL*/FLSHQFSFKYIF YSMKKLHLNLRHVLETVLSFPSSCY SSKFVHFALSFLFPSLSSFFCFLLFRF KFIFFL/RKSMFLSSNFPIFSILFYLPF F
1185	6682	A	1248	147	460	PFYKNCVSIVVVVFETGSCSVTQAG VQWHDFSSLRPRPPGSSDPPTSASR VAGTTG\MCHHIQLIF*SFFIETGTHY VVQAGLKLGLSSHPPTFSLPKWLGL QA
1186	6683	A	1249	168	407	ISHTREHSLDFFSFLFFFETESH/STR RLEYNGGLSAHCNLHLLGSSDLPTS

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						AC*VAGTTSIWQHVQLTFVFFFLIIIF
1187	6684	A	1250	163	396	TRFPILGSIA*IFFLFFFFFETESH/STR RLEYNGGFSAHCNLHLLGSSDLPTS AC*VAGTTSIWQHVQLTFVFFFFC
1188	6685	A	1251	37	698	RSSSPALEGGRKRVDMCELGSTIGP GPGSGQPACPLIWLHC*NPVEQAGP KP/PARPARSGP/QPPPTAGPA/PVGP KPPPTAGPA/PVGP KPLPTAGPARS WRP*PSGARGIKETHTEI*VP/PQGFF ACLIPTAPTGPTD**WLHLDLPTTP\ QPHPEAVQHTGGSCCLTPYDGP PPPQ PISSKHPLPSYTPSPKLPLEHPSQIL GETDFS NHQILVSHSLVSV
1189	6686	C	1252	150	308	MALQRTXLLLLLLLLTLLGLGLVQ XPMARMXCTSDSCGNTCTLRQVA SDRY*
1190	6687	A	1253	2	470	
1191	6688	A	1254	92	1047	RAAWQGGAEASGPPSALRGGSSALA AAARWGPAEEGARIPGSFFAWAAP AAPGAGAAAAPAPRADPGGRLLG EAGRGP NYAEAGTPTLHTLPRPHLR PCTHTHTRTPTPPRCKAGFKRTSLR FLPAPHHRTREEEAGEKQNFPLSC PFLRTCSEAEPPVLEEMVMGLGVLL LVFVLGLGLTPPTLAQDNSR\YTHF LTQHHIA\KTRGR\DPLSCKTFMRSR GLTSPCKDI\NTFIH\GNKRTLKGQS CEN\KNGKPLTEKNLKE*SKSFLSQV T\TCK\LHGGSP\WPP\C\QYRATAGF RNVVVACENGLPVHLDQSIFRRP
1192	6689	A	1255	199	792	PGSTAAADQSRNWNPNRVRKKPD LEGGCGTVLSGRWRSRRNRRTSGQ SLVPVYIYSPEYVSMCDLAKIPKR ASMVHSLIEAYALHKQMRIVKPKV ASMEE\MATFHTGCFICSISRRSAKR AMMIIRTSLEYGVRFINFPATEGIFT LCSS*GGATITAAQCLIAGMCKVAI NWFGGW HAKKKTCTVYVALYKAF
1193	6690	A	1256	1368	2229	WHPRQVL TGNDEVIGQVLSTLKSA DVPYTAALTA VRPSRVARD\VSVEA GGLGRQLLQKQPVSPVIHPPE SYND TAPRILFWAQNFSA\YKDQWEDLT PLTFGVQELNLTGSFWNDSFARLS\I TYERIFATTA\TFSFIPAHQRYPPSAR HWFTMERLEVHNSGSVA YFNASQV TGPSIYSFHC\EYVSSLSQEG*SPRW ARTQPSSWQMMLAQGFDPGFSTL MGEQFSYA\SDCGQASSSPGIWMGL LTSLFMLFIFTYGLHMILSLKTMDRF \DEHKGPTISLTQIV
1194	6691	A	1257	2	630	PDSSGPHRLRENPPWCLSPA\DKTN VK/APAWGKVGGAHAVRSMCAEAL ER\MVLFPPTPKPYFPHF\DLSHG\S AQV*GPRARKVADALD/TNAV AHR GTD/DCPNGVVPPLSDLH\AHKL\RV GPGSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVATSSLGTFPGFLVEA

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						PLLTFTQITFKGWKPRVGHAFALW ASPQPLLPFPAPVPPWSFE
1195	6692	A	1258	207	591	
1196	6693	A	1259	1	541	WNLSASPARQHPLLPHPVSCILLKPS SKKCLPNLTGYRFRVVSQKNMEDYL QALSSPH\DISLAVRKIALLLKPDKEI EH\QGNHMTVRTLSTFRNYTVQF*/ HVGVEFEEDLRV\DGRCQGCPCW HCNFSQSHELLSSRAMFSTAYKIQL ALHIHGFCIHSFSKLQMEKYL GKIKI KNNNTK
1197	6694	A	1260	214	491	ESHGAQIYIPHFCVPWSRWGNVRR CEALAVIYVTNNKIYVLSDEISCLQ PTSIN*QSNLLACK*GKN/RKTGQAR CHACNPSTLEGRSRIN
1198	6695	C	1261	48	173	MVRKRMEMKMRKLSQLRASGQLK MMRMXMSIPRSRRPRGIX*
1199	6696	A	1262	59	306	FGTDRTAVQTSSSQRCLCPWVAQK TYWLLVPSSLLKDLKEKKEVEEA* NGRDAPANGNAVSVCFAPWPQLP PHKIFPVLL
1200	6697	A	1263	279	889	TLAVFLIPCIGSPACPTMSDAA\VDT SSEITTKD\LKEKKEVEEA\ENGRD APANGNAVEEEDGDEDEEAESATG KAGQPED\DEDDVDYQGKQKTDE D*IRQQKRKKLNLKKKRP AHRGQC HPADDTRSPPPNPNHENLQQGREKR NQNFQGP A FLKSTLKRKFVCIFYL HFIFLYILLRVSHFLMISDDQTS LPER SLSYF
1201	6698	A	1264	358	508	DDVDVTKKQKTDEDD*TAKKRKV KLKKKKA AVTYSPTSRLRYLVFT FE
1202	6699	B	1265	46	386	XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKA AKL KEYEKDIAAYRAKGKPDAAKKG VVKAESKSKKKKEEEDDEEEDDEE EEEDXEDDDEEEDDDDE*
1203	6700	A	1266	263	484	
1204	6701	A	1267	157	886	TWKGKDLKKPRANMSSYAFFVQTC RGG\HKKKHDPASVNF/S/ESFSKKCS ERWKTMSA*R/EKGKFEDMAKA\D KARYER\EMKTYIPPQRGRQKRKF DSQLHPRGPPSGLSSSCSEYRPIK\ GEHP\GL\SIGDVAKKLGRDVGINTA AD\DKQPY\ERRAAKLKEYEKDIA AYRAKGKPDAAKKG\VVKAESKSK KKEEEEGEEDEEEDDEEIEE\DEED EEDEEEDDGLMKNKLGSGAVFFFSCL
1205	6702	A	1270	2	343	
1206	6703	A	1271	3	647	
1207	6704	A	1272	59	1297	NHASVQVKLWILSRSYLQLTMEAN GL*PQGLPDLKNDTFL*AAWGEETD YTPVWCMRQAGRYLPEFRETRAAQ DFFSTCRSPEACCELTLQPLRRFPLD AAIIFSDILVVPQMFSPPGTGQWKV TMVPGKGPSFPEPLREEQDLER\RD

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						PÆVVASE\LG YGFQAIT\LTRQ\RLA GTCAG*LAFAGAPMEP*MTYM\VE G\GGSST\MAQA\KRWLYQRPQ\ASH \QLLRILTD\ALWLPYL\GQVVAGA \QALQLFES\HAGHFWPHSSFNKFCT ALTSRDVAQAK*RPRLPGSQALATR CPCIIFA\RDGHFAPGRSLAQAG\YE\ VVGLDWTVPK\KARECVGKT\VT\ LQGNL\DPC\ALYA\SEEEIGQLVKQ MLDDFGPHRY\ITPHLGHLYPDMD PEHVGA FVDAVHKHSRLLRQN
1208	6705	A	1273	7	1047	
1209	6706	A	1274	7	960	
1210	6707	A	1275	3	53	
1211	6708	A	1276	237	441	AHFLHIVLVLLSCWYSV\RSRCTSQ QGVQSD\LAQLLPLRQRLEGEALV ALGAGVERRHVRPGRNST
1212	6709	A	1277	94	1003	VRVSLSLRLECNGAILPHCNLHLP SSDSPASASQVAGITGVCHHAPIFV LLVETGFHHVGGAGLELLTSSDLPA WASQSAGITGGSH/LCLANVKYFKS HFKIFVIDETWFQHT*LLSLSSCD*V *TSI*/PQVLD*NVLCPDV/SQ*LLPW LIKIFLKYTLDCW*KRQAWLYWY* FGTELFGCP*GRQTLCTFFLRSL/DS VAQAGVQ*CDLGSLLQPLPPRFK*FS CLSFPNSWDYRCAPPLPANFCIFSRD /MGFAMLVRLVSELLTSGDPPASAS QSAGITGMSYRAWPKPYAFEVECR PCDN
1213	6710	A	1278	4077	5102	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERPCKGGGGSRAAQ TASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASCKGRR/HTPSTINLFLNDPPLP KH\PH*ASPPTLGIEFQHEIWRGQTS KLSQHPSFSLRTLLTYSSQTAAFEFL FCRCLPTGHVPSSLLHSAADTAVSG DYATEGWECHCCWGCWEAKVGV LLH
1214	6711	A	1279	316	1180	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERPCKGGGGSRAAQ TASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASTQAAFEFLFCRCLPTGHVPSS/TP PFSSRYSSFRRLCLIFRGCWTEVLNE GGANSDSWSLTKLESGSSECS
1215	6712	A	1280	2	315	

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1216	6713	A	1281	195	739	KFSSRITVCHWKDVLLSGFQEPDRG SAMDYVRK\YAAIFL\VTLSVFL\HV LHSAPDVQDCP\EFTL\RENPFLLSPAR VPPILQCMGLPASPRAYPTPTKGPR KDGCWVPKEPSPSESPCLW*PKIHI NRGPQ*MGGFPKVGEPTACPLGS YLFYYPQIFKMFLPQVLSWMDWLDL LGIGKI
1217	6714	B	1282	29	200	MSRTRLVCPSLIPFCIYVVDVGFSPG PQSCTSHPEPKDIHAKCELAFLHHQR FYKNEGX*
1218	6715	A	1283	138	1908	ASRTAVARWECVLQNVRRPSPSR AWPSQLRPIASTATKCRE\CGPGYST PLEAMKGPREE\VYL\PCILPETQGT EGPRLSWATVDVDPKSPQYQCVIH\ RLPMPNLKDELHHSW\NTC\GSCF G*LAPSRGTK\VLPSFHLLFGIYVG GTWGSEPRAPKLAQGSLSPRDIHAK CNWAFLLTSHCLASGEVMISLGD VKGNKGKGFVLLDGETFEVKGTWE RPGGAAPLGDFWYQPRHNVMI EWAAPNVLRDGFNPADVEAGLYGS HLYVWDWQRIE\IVQTLSLKDGILPL EIRFLHNPDRCPKAFVGCALQAPNI QRFLQRTGGTLFSGRR*FQV\PPRK LKGWLLPKMPGLITILASPWNDG FLYFS\NWLAWGP*GKYDISDPQRP ALTGQLFLGGSIVKEGP\VQVLEDEE L/TSPSPEPLVVKGKRVGEGP\QMI\Q LSLDGKRLNNHHGRCTSA LGQSSF YP*SQSGERLLVNAGRVEW*DNSK KGA*KLNPQLSWVDFGEGAPLPK PLPH*ARYP\GG\DCSS\DIWILNSPPS HPHSLFWALHFPGGPGLSFCISLGTR TLGKHVPTTAKLRLWQCVES
1219	6716	A	1284	155	336	HFKIINRGWAPWFMPVIPALWEAE GG\HLKL**AMIVPLHSSLGDTVRL KYLCIYSLIF
1220	6717	B	1285	251	570	XELLVQLASLQTSFVTLDEAIKITNR RVNAIEHVIIPIRIERTLAYIITELDER EREEFYRLKKIQEKKKILKEKSEKD LEQRRAAAGEVLEPANLLAEKDED LLFE*
1221	6718	A	1286	83	977	HNQLTPVEEDTVESQFWSYCSLGCP AGDPSRKVIVRMSGKDRIEIPSRM AQTIMKARLKGATGRNL/L*RKKS DALTSFDFRQILKKVIGDLKCLMGE VMREAAFFTSWKPSFTAGDFQALT VIPKCSIKGGKLVSE/DEGKVIVRP VFTFASNFEHYH*RN*PVMELTGLA RGGE\QLAKLKRNYAKAVELLVEL ASLQTSFVTLDEAIKITQQAC*MPIE HVIIPRIERTLAYYSSQSWVRRE EFYRLKKIQEKKKILKEKSEKDLEQ RRAAG\RCWS\LLIFLAEKDRGSFL F
1222	6719	A	1287	1	3249	
1223	6720	A	1288	504	932	RYRCGVGSVLQAGGLILHLRKEGIL

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						HNKGKIEGMGLLEYVQGSLLQGW VMFVSVTAFFSLLFLGMFLSGMV AQIDANWNFLDFAYHFTVFVYFG AFF\MEAAATSLHDLH*NTTITGQPL LRDNQYNINVAASIFAFYDDS
1224	6721	A	1289	66	1363	RTAVMPREDRATWKSNYFLKIIQL DDYPKCFIVGADNVGSKQMQQIRM SLRGKAVVLMGKNTMHAQAPFEG TL*NNPSLWRKLLPHIRGEFGLLFH PGRTLTE\RD MFAGPIRLPTAARCW CQLPPCEVTVPA\QNTGLG\PEKTSF FPGL*VSPTK\ISQGAPIENPEVNVA ESRTGDKSGKPSE\ATLL\NML\NISP FSLWGWSSSQVFD\NASIYKP*KCLI SPEETLHSR\FLGGCPQMLPSVCLQ\I GYPTVASVPHSIINGYKRVLAL\SVE TDYTFPLAEKVKAFL\ADPSAFVAA APC/AVVAPPAAPAAAAAPAKVEA KEESESEDEDMGFAAAVLPGGTPK GALPPLAPGLALPRGPRCDPEAFRK RFRSQPRQDGGGHAELQKFTLPSLY FFSPKPSGCEPRANAKSSLNFVFSKY SLSTYYEQGL
1225	6722	A	1290	3	231	CSSSTSPSSEYCPSWGTEFRSGEMGS K*SSL*GASSSLSPDTGRGTGSSSSSS GGGGPGGVLGPLGCGLGGLPLN
1226	6723	A	1291	221	984	ETGLMCSSPLDGQNSV*RLTPWTLA PGTTAEVNQEDQKKSQIL*KKWQA AANSSRLVKNS*MP\T*KIQNGRMD KNSPTKYLLSSRDSS\THKESHLKD IALILPSSSEGSISELEQLSNSLPNKEL MTSICDCLLATLANSESSYNCLLTC VRTMMFLAEHDYGLFHLKSSLRKN SSALHSLLKRVVSTFSKDTGELASSF LEFMRQILNSDTIAPVCVAALSVM CSHRSAPTWFPPKGLKGARTTSRNS SEA
1227	6724	A	1292	817	1826	SCYPFCTS*KSFHSFCHTNDTVQSFK SI*LKR\SDT*SANRSSNNLITPACSS PVTP*APHSASEDTNLVPALSCRTFK AIGWRSATCKFKACMVQSTNWP SCFVFFNCK*LNPFIIKLGISSKAVTH FAPLSSLYKSKSSVNFTEASIAPEFSL SGP*SFILLISISKVVLYGQLKYKSGT SSLSYGSYVIGGTEAKSSAVYSTSKF GYLNVSRSKSAIPSSSLEICS*PSSPSP SSSSSPSSSSSSSSSGILSTVRRSSSS SSSSSTSTSSSSSPSSCCSSSTSPSS EYCPSWGTEFRSGEMGSK*SSL*GA SSSLSPDTGRGTGSSSSSSGGGGPGR SSWSPWLWSWRASIKLIFFLPISMF WDSFSNLGCGLGEGGWWRWEGGGG GRVSVMTLSLYPLDPYIASVRQLYQ PLSTRPSVFTFELGLKMMMEVFSSYS RLPNLSKTGALGLPYIVEE
1228	6725	A	1293	25	771	LDGPQGTSRPWGLPSLPPPRAGAGL SQGFSSSLRPARTPPSSGSKMSTEA QRVDDSPSTRA\QSSDGDQRESVQQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EPEREQVQPKKKEGKISSKTAAKLS TSAKRIQKELAEITLDPNNL*VAGP KGDNIYEWSTILGPPGSVYEGGVF FLDITFSPDYPFKPPK\VTFRTRIYHC NINIQGVICLDILKDNWSPALTISKV LLSICSLTDCNPADPLVGSIAQTQM TNRAEHRM\ARQWTKRYAT
1229	6726	A	1294	449	826	QKSRLIDDLFFFFFFCETGSCSVTQA GVQWHNHGSLQPPPPGS\NDPPTSA SQVAGVSVACHHSRVCARVCVCV CVCVCVCVESGLKLLGSSNSPSLAS QNARIIGMS*IVPKKLYFKSKVKGRI
1230	6727	A	1295	1	727	NTEDQRNEEKAQREANKKIEKQLQ KDKQVYRATHRLLLLGAGESGKSTI VKQMRILHVNGFNGDEKATKVQDI KNNLKEAIETIVAAMS\NLVPPVELA NPENQFRVDHILSVMNVPDFDFPPE FYEHAKALWEDEGVRACYERSNEY QLIDCAQYFLDKIDVIKQADYVPSD QDLLR\CRVLT\SGIFETKFQV\DK\V NFHIV*RGVQQRDERRKWIQCFND VTAIFV\VA\SSYNMVIREDN
1231	6728	A	1296	2	1271	PVRSSAPRRGH\SVASAPRSGLRQVA GRRGAALPCSLAPGCGAAAGASPC PGAGRRRAAGGRCLACECTSLTCA GESGKSTIVKQMRILHVNGFNGEGG EEDPQAARSNSDGEKATKVQDIKN NLKEAIETIVAAMS\NLVPPVELANP ENQFRVDYILSVMNVPDFDFPPEFY EHAKALWEDEGVRACYERSNEYQL IDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLT\SGIFETKFQV\DKVNFHM FDVGGQ\RDERRKWIQCFNDVTAIF V\VA\SSYNMVIREDNQTNR\QEAL NLFKSIWNNRWLR\TISVILFLNKQ\ DLLAEKVLAGKSKIE\DYFPE\FAR\Y TTPE\DATPE\GEDP\R*TRAK\YFIR\ DEFLRISTASGDGGHYCYPHFTCAV DTENIRRVFND\CRDIIQRMHLRQYE LL
1232	6729	A	1297	235	1571	GRPRPPPPQGRAPPPPPR\MGCLG NSKTEDQRNEEKAQREANKKIEKQ LQKDKQVYRATHRLLLLGAGESGK STIVKQMRILHVNGFNGEGGEEDPQ AARSNSDGEKATKVQDIKNNLKE AIETIVAAMS\NLVPPVELANPENQF RVDYILSVMNVPDFDFPPEFYEHAK VLWEDEGVRACY\ERSN\EYQLIDC AQYFL\DKIDVIKQAD\YVPSDQDL LR\CARVLT\SGIFETKFQV\DKVNF\ HMF\DVGGQ\RDERRKWIQCF\NDV T\AIIFVVGSSYN\MVIREDTGH\NGL AGRL*TS\PKGIWDNRWAAAPSLVIL FLTQK\EILLA*ESPLAGNSK\IKDYF PE\FAR\YTTEGCY\SRPGE\PHGV YRGQVTPFEDEF\LRSSNCPVEDGRH YCYPHFTCAVDTEN\IRRVF\NGLAV DIHFSGMHL\FSYAGAGFKEGEPPKF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NLKA
1233	6730	A	1298	176	505	ILKFPWIDIFLYSFNLVFLIFETRPHFILSPRLECSGMTSAHCNLCPCSSDPPTSAS*VAGTTGTQHHAWLI*LFGERELHHVTQAGLKLLS*VILSPQPPKVLGLQA
1234	6731	A	1299	310	326	SQHFGKLRRVHSLNSGVQDQPGQHEETSSLLKIQLARHGCVCVLAQLLRLGWEDHLNLGGRCNEPRWCHCTPA*VTE*DSISKNNNNN*QAGVQWHHLGSLQPLPPRFK
1235	6732	B	1300	99	430	XVITQRELVSQRQVSNDLTEQAATFGLILDDVSLTYLTFGKEFTEAVEAKQVAQQEAERARFVKEKAEQKKAEQKKKVEQKKAAVISAEGDSKATELIANSLAHRGGPP*
1236	6733	A	1301	64	967	NFRVEAGVRGVQQKETCAFKVLESI GKLG\LALS VAGGAENSALYNVDA GHRAVIFDPIPGQK*QDIVVGE ^{THF} \LIP\WVQKPQLSND ^{CRSRPRNCCQS} ITGSK\DLQNVNITLRHPSSGPVRQPSFPRIFTSIGED\YDERVLAVPSQLENLKS ^{VVAPFDAGELITQR} IELVSRQV\SDDL\TERA\ATFGLILDDVSLTHLTFGKLALTEAVEAKQVAQQGKQRRARFV/VLEKAEQKKAAIISAEGDSKA AELIANSLATAGDGLIELRKLEAAE DIAYQLSRSRNITYLPAGQSVLLQLPQ
1237	6734	A	1302	424	598	
1238	6735	A	1303	3	371	
1239	6736	A	1304	1	1596	
1240	6737	A	1305	2	556	WDMMYVTRFASFLRNVLPSFISDWLYVQKMNTWFKHENYGLMPLNGYLKMEIFFIQKRGALI**IYLSIKPSVKEFTETSAVFEDGTMFEAIDSVIFATGYDYSYPFLDETIMKSRNNEVTLFKGIFPPLMEKPTLAVIGLVQSLGAAIPTADLQAWWA ^{AKVFASRWAILSFIHFI} NEHLLNTCY
1241	6738	A	1306	955	1187	IFFFFFFFKMESC ^{PFAQAGVQWCDLG} SLQALPPGFTPFSCLSLLSSWDYRRPPHLANFLYF**TWVFTVLARMVSI S
1242	6739	A	1307	6345	9041	
1243	6740	A	1308	236	437	LLTLRWSHSSHVLLKTRGQPRRSGWCL*SH/HFGRPRRADHLRSGVQDQPGQHSEIVSTKNTKIGWAWWQVPVIPAT*E
1244	6741	C	1309	182	433	MHLDLFLNKTLPQIRGVESEQSSRLHPLPDPRGDRHRMADNLPMEIHGSATSSGKPSDFNQA ^{AVDGAGERGG} KEVLGGTLDVL*
1245	6742	C	1310	72	254	MVSTQLRQASDPRTTIGRERFELLRRVDKLMSPRLPTGTLNPHHFWTLSIPQVGRCNAP*
1246	6743	A	1311	225	735	GELRVNSLHVSTHFQIPEETDIGWL

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						VSPGQGPAPPFEDIQLWPPGSLMAA EPTDQSLEESH*DRWITFFTFAR\Q EGRK\D*PQRSNEFKE\LVTQQLPHL\ LKDVGSLDRKN*GAWDVNQDFGG SRFN\EY\WRLIGGAWPKEIRKEEKT LKIQUERSKAAWLEDGVGQGR
1247	6744	A	1312	165	629	TGEMLIRKHCLYIVCKLSLLFIFRDM SCSVAQ\AGMQWHATNAVDGD*LT ASLKLLGSSNPPPCNPKRAGIIGMH QHIQLIFCWSFF*KQAFLRITKALRN FKKI*FQNTLVTKY*HCSLTFFFCH FNENRILHLLAQMAKQDSGLLRV AWEA
1248	6745	A	1313	76	523	ELGRNLWNASQGRGLEWVSNRKF WAVYAYITFLSHPERVVNKHNCPL FE*KGECWEW*EARAQTDRVQKQ MWLLRIQTSFSSRKETQSLRVTFWR YPVSPSPISMR*MSPGNSYRTLYKR NVPLKAHFPTAVLAVVPPAVTNQG KEQG
1249	6746	A	1314	55	391	
1250	6747	A	1315	996	1334	WASVGLSGPRSPSSRPQ*ARPRPG APASLRQADLGRGWRDLGAPRPR PPRTGGWRSCCRGRGPGSRPRGAR AGLPGAPGGWRRSRRSWTRARA ATRPAAAARGSRTPRG
1251	6748	A	1316	1	993	
1252	6749	A	1317	72	496	PPWARGSARRPPAWRTVRMPSCHP RMFGAPQKTFLRVSVWSRCRPWGI VMRMM*PMRGQVRRHNSCMAPKT EE*NPTVSATFCCCSFVSCSWPPVTR YSSILFTAAM
1253	6750	C	1318	202	378	MTPYLTLFLSPLPPKGEIWGLLLFLT PLGFLPLSLPLLLPCPAPAGVRRQW DGPTEGA*
1254	6751	A	1319	1	1541	
1255	6752	A	1320	9	345	YLSEVGVSVGIVIRPRQWIRPEGDP FHGGRLKMDPLRAQQLAAELEVEM MA\DMYNRMTSACHRKCVPPPFKE AELSKGESVCLD\RCVSKYL\DIHGA *WGKKFDRVLLQG
1256	6753	A	1321	199	985	VRGSGADPGGRLCSASVRRGGPLE GAFNSRTRQATMTENSTSAPAAK\P KRAK\ASK\KSTDHPQVFQT*IVACN SSPRRTGAGS\SRQSIQ\KYIKSHYKV G*ERLTSQ\KLSIKRL\VTGVPSRQ TK\GVGASGSFRL\AKSDEPKKSVAF KKTKEIKKVATPKKASKP\KKAAS KAPNPRNPKSSPVKKA\KKKLAAPG PKKA\NKPCTVKAAPGKAFKAHWR PYLV*PKCKCPVAKEGRARRKLTMI VFFLRDTPSWSPIFCK
1257	6754	A	1322	3	129	
1258	6755	A	1323	376	545	NILHRLFTFREKTSYAPFVRRFHSK GRHTPPALKWEVWVRKKGPGE DSDMALSYSPPPPPPPMVGM*/SP PSH*PLLLCRRVKKEGF

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1259	6756	A	1324	14	262	FQTQTKYQAPLHPAPGHRPTPLPPP PPASHCHLFLWSVCKRSNKPQAPFI SP\PPSNPLPEPGPCSSLCQPWGRTG EGLAPPD
1260	6757	A	1325	234	275	
1261	6758	A	1326	52	454	SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKL RVPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLTSKYR
1262	6759	A	1327	3	616	PTLLVPTDSERTHPWLLSPADKDQR QGPWAG*G*GSHPPSNVAKTLER/M VLFPPPTPKPYFPHFDLSHGSAQV\ KGHGK\KVADALTNAVAHVDDMP NALSALSDLHAHKL RVPVNFKLL L\SHCLLG*PWAHLPRPSFTPCGCK ASL\DKFPGLFVEAPLLEPSKLPKL GSLRLAMLLCPFGFPQPLLPFAPV PPWSLK
1263	6760	A	1333	732	1634	RRFWQVENHEILTEQAFVGQKPIFR/ MKSLKEKLTATKRKPKNIGDILT KRKNNRTGSEAGEPQRWPRRCPI RRAQEKNSQRPRKREGKVPIWRK KPLKTGRDRSW*P*KLLALCPSTVG IRSRAG
1264	6761	A	1334	1	531	FFFLHVVAHLIFTATQMGSNITITVL QMRSPRRRVEYLAQDHTPFATPHS KSHRQLRLSTSMVITYHLPLQTISS LVPYSQWGHLSQSPGPKLGNRKPF LTPSPSPTPSKWNP\SPGTMFFRVLI QSPLSSPRPC*PIVRCPAAAPGSSLP STLFAGPSPPFPASYTLRLRCF
1265	6762	A	1335	130	361	GACCPSPGGESGT*C/SPRGPRKPS GPSPKAKCS*QSTGCGCASSPPSPS PGRAPCDSPILACDLGQGGFLQLHT H
1266	6763	A	1336	144	224	
1267	6764	A	1337	1111	1200	PGVVTLGGGACSEPRCATALQPGR ESETLP*TLHSHNQSKPLPPICYPI S VNGNFILLVAQVKKPCKAGCGGPR L*SQHFGRPRQADHLRPEVQDQTG QHKGKTASL/LKNTKISQVS/WTLGG GACSEPRCATALQPGRESETLP
1268	6765	A	1338	344	512	ETLYTME*YTAIEKNEIMSFAGTWL ELEA\VL\SNLV*EQKTKMLPCSP L MGWELK
1269	6766	A	1339	274	393	
1270	6767	A	1340	1	561	VRSAVGGTGMSSGASRKSWDPGKP WPPDWPTGRK\MK\VLWAALLVHI SCQNPMKPW*QAV*NKSRSPELR\Q QTEWQ\SGQ\RWELALGRFWDYL RWVQTLSEQVQEELL\SSQVTQELR ALM\DETMKE\LKAYKSELEEQLTP V\AEETRAR\LVK\EPQAAQARLGAD MEDVRDRLVHYMFVDV*AI
1271	6768	A	1341	1	746	MAAAGAFRLRRAASALLRSPRLP

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						ARSCRPRPDSITRSPDVRLPLEKQL KNAINQRGTKGPYIRYYPEVVDHY ENPRNVGSLDKTSKNVGTGLVGAP ACGDVMKLQIQVG*KRGRFVGC*G FKTFSAVGSA\ASSLSHLNGVKGK T\VEEALTIKNTD\IA\KELCLSFPWK LALAPMLGLKVAFKAALADYKIET RTQKKGEAEKKWSPPLGEASSRPTP AVPQPAVPVTLDVSGSRLPSPTEGA L
1272	6769	A	1342	160	381	SWGLDSALGVSDTTHHPKVVGRAK HRGFLKWLP PPPG PPLGKRNCQYP NP\QLPESGPPQQYFYLKCCPFYEL
1273	6770	A	1343	653	814	WDSTPLSSFTDWMLWPEKRQVGA CSHPTPNFL/C*GKLNISPNSPCQPKV LDLT
1274	6771	A	1344	954	1245	DLSLTTSRQRKHEFKEVILPNYTHD KLYLINSNHPTKMCP*NOVLKKLIK ITQQWTGAMIHAYNPSTLGGRWG WIT*SQELETTLPHIRGTLHKI
1275	6772	C	1345	155	431	MRERGLGPLGVFRSDAGLKS LPEG RRESGALEECVIHTQRVCDWKVPE HPLAPLLLVSVAVLRILAKPLPTQR DLFLLLSRSSLFNQHFPLC*
1276	6773	A	1346	2	70	
1277	6774	A	1347	1	271	LFF*TESCSVTRLQCSGMISAHCNLH LPGSSNSPASASRVAGTTGARHHAQ LIF/VVFLVETGFHHVQG DGLDLL/N LVICPPRPPKVL*LQA
1278	6775	A	1348	117	229	KKTMFRQKLFYKRKQLQKGPRP*G SAKKKLCFGKSYFIRGSSFRKGQGH EERGLKYKKKTGEGV
1279	6776	A	1349	255	381	IHFSINSQLFSPSSPPNKKG*FPKVT* KR/P*NGPRYIPQRF
1280	6777	A	1350	72	577	TTGVRGALQREGGSLPTQPQGERA LGRRRNQPA GD P GFA\G*RG A*WP TGCKQGRGGSPSPQPLGSGGR\QNL ARLKPPRPPP/PQEGGDKGRPRQQG PSWRSKSSPPILPTSYPGGDKGVVP KHKLEAVNSVRARSSVRNKCWSN RMDIALRCPVTVAHELTYS DAL
1281	6778	A	1351	160	336	
1282	6779	A	1352	1625	1920	LSFPAKKGNDCLPHVPGLSFKGRVP ESRQEFCE TQESSLENPRLCIPV/CHP WAPWRWEPGETAEPPVLRKEAF* PGPPCPPPNRVSETREAVLLQPRI
1283	6780	A	1353	9	249	KVHTKPR TSSICRSHIGFLFF*ETES CSVTPPGVQWCN LG\SLQTP/PPGSS DSPASAS*VAGTTGMHHR AQLII*F YVFTGFFWQ*QLSDGILTH
1284	6781	A	1354	426	744	DNLLKSFHLIISINCLFFCFFFL*TESC SV\SR LKCSGAILAHCNLC LLGSSDS HISASLVAYRCLPPCQANCFFSFLAE TGFHHVVGQAGLELKIQLAECSG MRQ
1285	6782	A	1355	184	422	GYIQGSPALVSTHGGHAV*PPTQSK PTEHAHP LQPRRWARTRV GEGIPC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AHPSPSCSPRPLATQKRFQANRRGR LEGLC
1286	6783	A	1356	3	1221	HFIYLFIFIFLRQSLALPLRPECSGAIS AHY/RHLCCLPGSSDPPN\SASRVPGT TGMPCRTWLIFVFLVEMGFHHVGO AGLKLLTSGDPPALASQNGGITSVS HRVQPKNFFE*SRYYLNFKGN*DS KRLKK*KIRQLEN/RRNMIQILLFF* L*NSCSRMKDNS*AREKYLQHILRG LRFLTCKDSTKLDLKATNRNTTLE* MENMMKQFTEEKIQMPNKDLKRC* TSLGVREMQIEVIRYYSRSS*QKFK RVV/IIPGQLQRKCQF/PCTW*KSKPL KRFSEEI*YNINQIHLFEAGSCCVVQ DRVQ*YHHSSL*PQPPRIKQSFHLSL PTSWDYWHMPP/HPS*FCVCLFCFF SRDEVSPGCSSWS*TPELKLSSHLNL PKCRDARPEPPCVAQYDINQNCKK HVLS
1287	6784	A	1357	703	918	TREVEVAVSRDHATALQPGQQRQD SVSKKKKKGRVQWLAPVIPSTLGD QGGWIT*GQEFETSLTNKVKPHLY
1288	6785	A	1358	273	561	DRQAEKKRNIL**NEIVLDLPR*PHT AS*ISSTT**FENTALRPGVVAHACN PSTLGGGA/GQIT*GQEF\ETSLANV VKPISTKNIKINWEWWCRL
1289	6786	A	1359	375	663	LITKQLGLGVVAHVCIQHFGRPRW ADHLSPGVQDQPGQ/QGETQSPQK NTKISQVWWHVPEVLAP*KAEAKG LLEPGRQRLPPTLHSRLGGSETL
1290	6787	C	1363	79	153	MPDMIRQHSSCLIKRVYLTRWFGR*
1291	6788	A	1364	4776	9134	WLHDSVNILKNIEHFFFFFFWRQSL APSSRLECSGAISAHCNLHLPSSDS PASASQVAGITGAHHHAQLIFVLV ETSSHHVGQASLKLLTSSDPLALAS QNAGITGMSHHTWPNH*IEHF*WV NCMVWEHYLNKAILKFYKEIKSRR DPTPKAYLIWGR*C*/TVL*NKEQVT DTKFLT*LFKGVGRM*KFTVPAPFV VRVS*LYLA*DKCLVIIVAMLMDRN VIFLKGPLMGFVG*LCSGFQGGKEWF LFESYPSLPTSPTTLSPALPKYFL*VN VTKANFLQ*SIPFYIMVLTFFPST*S QYTNFFFFFF/HFFFFFF/CFETESH VTQAGVQW*DLGSL*PLPPRFQ*FS CLSLSSWDYRHAPLRPANFCIF**R /SGVSPCWPGWS*TPDLK
1292	6789	A	1365	3	287	
1293	6790	A	1366	75	301	AHKKLRAAPLAPMTGTH*K\VFVK AGDKVKAGN\PSWVMFPMKMEHTI KSPKDGTVKKVIFYREGAQANRHHS FSRV
1294	6791	C	1367	155	377	MKASSFKKLQKFYIDPYKLLPLQRF LPRPPGEKGPPRGGGGRGGGGRG GGGRGGGGGGGFXXXXXXXXXXGF RG*
1295	6792	A	1368	363	423	SIKGTENGFLIVL*PKSQV

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1296	6793	A	1369	157	723	KTLWRYGNRG/GFQRGGST/RAGGC /GAQQQGPEGHVAPY*GEVFLHPCE DDIVCKCTTDENKVP\YFNAPVY*E TKEQMGKVDAIFGQLRDFYFSVKW SENMRLSSFKKLQKFYIDPYKLLPL QRFLP\RSPGEKGPPK\SGGRGGRGG GRGGGGRGGGRGGGFRGGRGR\EG GGFRGGRGGGFRGRRTLSETC
1297	6794	A	1370	1	810	ASPPLVCTHARSFSVLAPFLHFPLL PDRRSRSFRAVHFWGPRSSPPHAAV RLREARRGRDRREKAESPTGEKSTS PSSRRQRGPPTKVRPPAPFTMQP ASAKWY\DRRDYVLKWEFVFLNTL RD\NVNF\EKSKTYNFSCGG\SDN F*GILNEIDLH\CID\PNDSKHKRT\D RSIL\CCLRKRRIWASSWPKGLTK\E RGKGLIW\SVDFN\N\W\KD WEDDS DEDMSNFDRFSE\MMNNMGGD\EV VDYPEVDG\ADDDSDSDDEKMPD LE
1298	6795	A	1371	1	588	
1299	6796	A	1372	179	989	KWRNQSWRWPKPGTNWMLSCSVC WRRVTWTGSVWMRKLGKHPQTPT /IKDCSIAATGKRPSARFPHQRRKKR REMDDGLAEGGPQRSNTYVIKLF RSVDLAQFSENTPLYPICRAWMRNS PSVRDAECSPSS\PLPLPEDEEG\SE VTNSKSR*CVQACPPTHPTGGQPKN ACR\SRIP\PLAALRMQGT*RWSPF EPEPSPSTLIYRNMQRWKRIQRW RPPACLPLVGPFAAESPLCLSRWK EASHRNQLRYSESMKILREMYERQ
1300	6797	A	1373	245	336	HIPSQGDGK*VKNRARKIVSYSRG GWHSG
1301	6798	A	1374	127	872	EATGQTVGTVPSSLSRPRPLHSSSG GVRIQTLFATSRPLDKTASIFLVLSN ACIF*KILIA*KEIQDS*SHH*K*LLLI RLDFLSSFFP*LIN*FFFFPGNSLVH RLFFFFNLGMVAHTYNPSTLGGQSG RIA*A*EFKASLGNLVGPHFFFLGGG VGKSPFIKILNKKKTKSLQKKKR YRKRIPLLHMVPKREKNKGDNRQH AQQIKASFSYFFNVQNTSKGYTYLK QELSDAGHAGPGKPFQ
1302	6799	A	1375	37	80	
1303	6800	A	1376	1452	1700	
1304	6801	A	1377	316	373	
1305	6802	A	1378	144	356	FQFRLTSLRNSTDVHRCPLPPPP\S PPYPGPWGMGCGRFPKGQGGPRP PRLSGLG*FLSFFALGFSDG
1306	6803	A	1379	860	924	
1307	6804	A	1380	263	616	TTCFSFESRASCHFHVASAVSPPTPL CSPATLMAQDKAGKPSPRK/PSLAP EKPLSPLSPQ*RHSPKPKAPHVESP SGSPSTRAKKR*\FSSPPSLWGQEP GHAECPLPYLGEGAPA
1308	6805	A	1381	152	272	YSVLKFNYEILKNCFSSFV*VSEPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KTIILVYFTLTEKL
1309	6806	C	1382	71	316	MCHHSQTLFLYFVKTKSHCVAQAG LELLASSDPLDSTSQSVGITGMSHH TQPLILFFNFSVSVKYTKIMVLKNGF RNSYKK*
1310	6807	B	1383	165	520	XNLKLIDNWDSVTSTFSKLREQLG PVTQEFWDNLEKETEGLRQEMSKD LEEVKAKVQPYLDDFQKKWQEEM ELYRQKVEPLRAELQEGARQKLLP VLESFKVSFLSALEEYTKKLNTQ*
1311	6808	A	1384	3	558	
1312	6809	A	1385	3	118	
1313	6810	B	1386	28	384	MKAAVLTAVLFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK *
1314	6811	A	1387	2	1093	GGASCCLPRSLWLPSSRFRPCPRPG LWVPEVFSRSVPFSSPGCNEWGSTG LLHAEGTPLSQALLLQVPHGPFRM KAAVLTAVLFS DG*ARRRHFWQG G*SPPRAAWDRV\KIDLATRPWTV LKEQRTETYVSQFEG\SALGK\QLNL KAPLTTGDSVDLPPFS\KLREQF\GP C*PRDFLGINLGKRETEGP*GKGR*G KDLWKEVKAKVAALTLDDFQERS WQEEIGAFTRQKV\EPLARKNFQEG\ ARPESLHELARRSLSPLEEMRDRA RA\HVDALRT\HLAPYSDELQRQLG AR\LGALENGGARMGQYHA\QAT EHLSTLSEKAKPALEDLRQGLLPVL ESFKVSFLSALEEYTKKLNTQ
1315	6812	A	1388	1	2076	
1316	6813	B	1389	560	752	XSVAAVTALNSES NFARAYA QGISR TKYWELIYEDSMDLIAKLPCVAAKI YRNLYREGSVTRGH*
1317	6814	A	1391	1031	1407	CVGGRAQVEKEGAALRLRPATVPR ALMSLSSLVKPETA/ALCGTEMQDF FTPLLCDFKSPGISFCKGT*MCLRSC *HNVRRWR/DQPTPVSTVTPVPTLT CVPSPHIFVPER\GAGCLHLCLKFM VH
1318	6815	B	1392	97	880	MAPRTVLLLLSAALALTETWAGSH SMRYFYTSVSRPGRGEPRFISVGYV DDTQFVRFDSDAASPREEPRAPWIE QEGPEYWRNTQICKTNTQTDRES LRTAARLLQPERGRTMYGCDVGPD GRLLRGHNQFAYDGKDYIALNEDL SSWTAADTAAQITQRKWEAARVAE QLRTYLEGTCVEWLRRYLENGKET LQRADPPKTHVTHHPISDHEATLRC WALGFYPAGDHTDLAAGMPRTKL RNTELVETRPAGR*
1319	6816	A	1401	1380	2180	EIQSEWNLQDL\ELQLEERLAGAWE E/LSFRAVRMPSPFRSSALMG\MCG SRSADNLSWPFH*NVMEPVTELM

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						QEQSYLKSELGLGLGEMGFIPPGE SS\ESV\FSRAQQDSFCECSGPSNATR KMGVPS\TASVGKSKTPLVARKKV RASVALTPTAPSR\TGSVQTP\PDLE SSE\EVDAAE\GSPRKL*GPKSESEV/ EKEGHGKLP\MPAAEEMHK\NVEA RLSLQQVIR\EIKESIVGEIR\REIGKL DFWAAVSS\SKASNSR\QDYH
1320	6817	A	1402	119	301	INDKRKKKRPAPRGAGGLHLQLCL SQPPQPRGHPAPIPTGQAGPRDSGP GASP*/GRDPPSD*WTPADLGSDPW AGPLPTPQEP*GSRWPSSATVSLSAS TATGTPCTYSHGTGWTQRLWTRGL PLSRDPPSD
1321	6818	A	1403	1451	2495	RGLAGNFEDRKS AHYVFQTFRGGE RRSLELEAHLEGWSLGLRFLGLPLK GPPA\QGHFHPSLPISWRGAGVPHS R/SPFPTLGIPG*IFPPKPGRPRGPPR KEDLPGPMVG/RPSGPLPQLPSAVL SADPAGPRPHVPFCEP/SPSHGVRAS PGSKWVEEEIGGEEGRQ/PKCRQAF QEAWLMQG/GARGQGLPGS/GCWR INKPSKPSKRGGKGLTCQTFSTNIC* SPPLMPRSLP\GPSFILHLISSQQP*SG LLFIDPIPPEKGRGGLSERWGRAFG DSVACSFQKPTPGPWEVFEQDAWP NPWP/QGPPPENFPKGNPSHSRNIHK GDEQSPVRTKTEPTPWGGKHSQFA SR
1322	6819	A	1404	3222	5798	PLLTPLVSKVTAAGVPLFFFFFFF* DIVSLCHPGWSAVV*P*LTAASNS*\ VKQSSHLSPSSWDNRYAPPRPANY FYFYFL*RLDLALFPKLLLNCAWQ VILPSQPPKVLGL*AQSSGGIHSGL SLSPCFLLCNPI
1323	6820	A	1405	38	402	
1324	6821	A	1406	2	380	
1325	6822	A	1407	1	477	
1326	6823	A	1408	1	1104	
1327	6824	A	1409	524	1584	IVKMEKYSIMKSMNMHLTERKKDH FRNDTNTQSFYREKWIYVHKESTKE RHGYCTLGEAFNRLDFSSAIQDIRTF \NYVVKLLQLIAKSQLTSLSGVA\QK NYFNILDKIVQKVLDLHISLLFKDL PQVLSSNLCTLIRGVGKSVLVGNIN IWICRLETILAWQQQLQLQMD*G K*TMGLTL\SDLPLAHGWNNILLPV FQDGWGHSFTFRPR*PPRLYMAVG EDRQLWKKL\CQYHFAEKQFCR\H LILSEKGHS/VEWEVGCNFAFRKH YPAKEQYGRQHCFRCRHSILFWKD SGHP\CTAADPDSCFTP\VSSQQFIAL FQVLRACPLPIPYWRFVNPCCPVQG LIVSVL
1328	6825	A	1411	588	855	VLLSSYLTYSLVFICWLFICLFICIFI FMYVTM*IWFVAVFVWNLVFPYKV VK/TPWRSRIHVHCLYF**NYSPIAF

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						LYSA*CYSLCVH
1329	6826	A	1415	277	509	YMLSCHHTFVQTHRMYNTKHEP*C KLWTL C*DNLSM*VHQL*KFPTLVG DVDS/ERRLCMYGDRGYMGNLYIL LSILL
1330	6827	A	1417	15717	16041	
1331	6828	A	1418	41	544	TKLVMMQKLLKCSRLVLALALILV LESSVQGYP\TRKPRHQWVR CNPDS SSAHCLEEKGHMFELLPGESNKIPR L\RTDLFPKTRIQ\DLN\RIFPLSEDYS GSGFGSGSGSG\SGS\GSWFLTGNNGN RNYQL\VDE\SDAFQ*QPLGSLDRNL P\SDSQDLGQHGLEEDSMV
1332	6829	A	1419	168	467	
1333	6830	A	1420	2	196	ASTRRRSGSRGLTRRAAFGV RAGE GWVCGGPAGSRRRRKLPLTGP GSG SFQCRSRGGRGSVNMGKDPNKPR GKMSSYAFFVQTCREEHKKK\HPD FSVNF\AEF\SKKCSER\WKTMSCKG RSSKF*RIWAKS*QSF AIDR\EMENL RFLPKGDKKGKKKDPN\AP\KRPPS AFFLFCSEHRPKIK\IEHPGLSIGDTA KKLGEMWSEQSAKDKQPYEQKAA KLK\EKYE\KDIAAYRAKGKSEAGK KGP\SRPTG\SKKKNPPRSWRGWEG *EA**DPASGIWGAGRRGLGLWRA GGQSEEAETAPDRARFWEFSMSVT RWTRICQHG
1334	6831	A	1421	3	107	
1335	6832	A	1422	450	851	KTEFTQNYFWKSCTGVDGFFFSILF CLFV*DGVL LCHPGWECSGCDLHS LATSASQVQAILVPHQPSK*A WDYR RAPPQLG*YLYC\CRDRVFTMFVPG LSNFW\PHV\HLPQ\PPKVLRIIGREP TCAPASMAF
1336	6833	A	1423	6	461	AEMTPLHSSVGSVRVRLHLKKNYI KKPRKALFISIFGIIFFHLYVSTYIYL STFSFTSLILMEFILCVV*VLHLQLK NAILMAYWY/TFILITWLPSEEDLK VL*LFMPKNELIFSKCFHFLFIVPKFT LLDHLAFLRLKLAFWRLGW HST
1337	6834	A	1424	222	350	GAHTWTGISQAALQPTAPGRLSRTL LFLC*KCGEICNLLSGC
1338	6835	A	1425	198	385	
1339	6836	C	1426	207	385	MFFYKLAQMXQISVSTLKFKLVLFV PTGXQVNGGEPSTLYGRWGRXGSA PSWRYQFPCP*
1340	6837	A	1427	327	516	
1341	6838	A	1428	58	255	FSPDFYRGYIYFYHYFGFEKFFFTPS NFFISQSR*FFCVKMFSFFNLRFKIPL PNHVDFA LCFFVV
1342	6839	B	1429	242	509	MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DXGENDLEVKEENGVLVLNDANFD NFVADKMDMTARDLPX*
1343	6840	A	1430	338	511	NSFSKSKTPCVAHGRGVHAEAGNK RQYLGFLFFFF*FFILWCFTSCSEY

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1344	6841	A	1431	2	454	
1345	6842	A	1432	671	955	FFFF*IFTLGCFTSCSEY*ITMNDVK* FSPEFLPEGYLLFLSLFGV*KIFFYTL LISLFLKAD/RFFCVKMFSFFNLRFKI PLPNHADFALCFFVV
1346	6843	B	1433	46	3152	MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLFEYAPWCGHCKQF APEYEKIANILKDKDPPIPVAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEVFDEVVNDADIIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDVVIIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQGGQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSAIDFVLKYALPL VGHRKVSNDKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEVAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFFKKGKLPVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLIIFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIAKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEELMDVQGSTQDSAIDFVLKY ALPLVGHRKVSNDKRYTRRPLVV VYYSVDFSFDYRAATQFWRSKVLE VAKDFPEYTFIAIDEEDYAGEVKD LGLSESGEDVNAAILDESGKKFAME PEEFDSDTLREFVTAFFKKGKLPVI KSQPVPKNNKGPVKVVVGKTFDSI VMDPKKDVLIIFYAPWCGHCKQLE PVYNSLAKKYKGQKGLVIAKMDAT ANDVPSDRYKVEGFPTIYFAPSGDK KNPVKFEGGDRDLEHLSKFIEEHAT KLSRTKEEL*
1347	6844	A	1434	785	1271	LCTDQLHNFNNYFQDKDKCFYFPM FWSFLGLETEAACFKPDSKGKALQ NRKYFN\VYLPSATSRDLWISPGWS QFFFFFFFFFFFFFF*RA
1348	6845	A	1446	549	791	GLLSN*NFFFSILIFFFQTESRVA\RL ECNGAISAHCKLRLPGSRHSPASAS RVAGTTGAHHHAWLIFVFLVETG FHHVSQDGLDLL\NLVIHLPRPPKVL G*QAGVQWCDLRLQAPPPGFTFPS CLSLPSSWDYRCPPPCLANFFCIFSR DRVSPC
1349	6846	A	1447	59	485	NSPCSGSSIATASPERRKGINPAPPST PAAPCRS*ACTAAAAAAVR\DDRLN VTEELTSNDKTRILNVQSRLTDAKR INWRTVLSGGSLYIEIPGGALPEGSK

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						DSFAVLLEFAEEQLRADHVFICFHK NREDRAALLRTFSFL
1350	6847	A	1448	125	927	NPPCSGSSIGPCSPKRRKGIKPGPPHH RKPAPSGS*ACTAAAAA\AVRVPGS PSTAV\VTRVRG\LGAPDAPHPLK DPRVGEGNSQRNPNL\ANLFYSDD RLNEQKEL\TSHDKDEHSRRPSSRLT DGKTPLNWRNNC*SGGSLFNIKPA GRRWPEGSKGQLLQFLLEFA*GATC GADPKVFICFQTRTREKAEPPLLRV FSFFGLCRLVRPGGIPLVPKETPDAC FMALQRSRESLPGEVEEVGARLRG WAIPPPWGHPLVCTGG
1351	6848	A	1449	1	866	ESVDLAAEAVRIRRSPLIFSKAVHIM AAAFRKAASRQREHRSRQPGFR KHLGLLEKKDYKLRADDYRKKT RITSKALRK\KALEK\NPDEFYKMT RVKLQGWSYILLRETKGRK*PQEQL KADEELQDVKYIEMKRVAEAKKIE RLKSELHL/VWDFQGGKQKNKHVFF FDT\KKEVEQFDV\ATHLQTAPELV DRVFNRPRIETLQKEKVKGV\TNQT GLKRIAKERQKQYNCPAHQRIE\RE KKLIPLLPQKIQTRKDLMDKTQKVK \VKKETVNSP\AIYKFQKSVENR
1352	6849	A	1450	3	896	LRAVRVGLLLGGGGVYGS\RFR\FTF PGCRA\LPWRVRVQR\RRCCEMSTM FA\DTLLIVFISVCTALLAEGIT\WVL \VYRTDK\YTRL*AEVEKQSKKLGK GRKET\TEFSWFGQKKKIERQEEE T*RNNNRDLS\MVR\MKSMFAIGFC FTAL\MGMFNSIFDGRVVAKASF*P LFSYIQ\GLSH\RNLLG\DDTHRLVPF IFLYILCTMSIR\QNIQK\NLGLAP\SR A\ATKQGRVDFLGPPPPSGEVLLEL KELFIFYSFLLGH\THIRMGQLFCSQE PIGSLYYLGLFLVLNYFLSLLGYD
1353	6850	A	1451	2	125	
1354	6851	A	1452	18	1374	LAEQIVPRGVGIRPPDKADQAPCRS PIRTPAPESWHCDSRQFRQDSSRM KMRVLGLVCLVLWTLHSESGG KLTA\DPETNMNVSEIISYWGFPSE EYLVETEDGYILCLNRIPHGRKNHS\ DKGPKPVVFLQHGLLADSSNWVT\ NLGNSRLGFILADAIDVWMGNTR GNTWSPKHKTLSVSQDEFWAFSYD EMAKYDLPASINFL\NKTG\QEQQV YYVGHSQGTIGFIA\FSQMLELAK GLKMFFAWGPVASVAFCTSPMAKL GRLPDHLIKDLF\GDEEFLPQSAFWK VAGVPHLATHVIL\KELCGNLCFLL CGFNERNLNMSRVDVYTTHSPAGT FVQNM*HWSQAVKFQKFQAFDWG SSAKNYFHYNQSYPTYNVKDMLV PTAV*TGGHDWLEDVYGVNI*LTQ ITNLV\FHESIPEWEHLDFIWGLDAP WRLYNKIINLMRKYQ
1355	6852	A	1453	165	1353	LPKPRLGPGQPEKDRTESSVRMAIT

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						LEEAPWLGWLLVKALMRFAFMVV NNLVAIPSYICYVILQPLRVLDSKR FWYIEGIMYKWLLGMVASWGWYA GYTEMEWGEDIRAVSKDEAVTLV NHQATGDVCTLMMCLQDKGLVVA HMMWLMDHIFKYTNFGIVSLVHGD FFIRQGRSYRDQQLLLKKHLENNY RSRDRKWIVLFPEGGFLRKRRE\TSQ AFAKKNKLPFALTNTVTLPRSGPTKIIL NALVAQQ\KNGSPAGEDAKELASK SKGLQWIIDTR*PYPKAEPI/DNIQT WVFGYRKPTVTHV\HYGIFP\IKDV P\LETEDL\TTWLNQRFVEKEDLLSH FYETGAFPP\SKGHKEAVSREMTLS NLWIFLIQSLAFLSGYMWYNIIQYF YHCLF
1356	6853	A	1454	313	650	FVICV*TYTGMNTHSPHTKTL SFLS DSG*FFYCRSL/CNIG*KQTYPPQNR LHTHTHTHTHTHRGYFSHTSSTVEK ALLTRIEGSEEDNGFYGWALRTI LVAFKSQCMH
1357	6854	A	1455	2	401	VSVGGLVGEVACACRDCIPETMAE GDNIRSTNLLAETASLEEQLQGWG EVMLMADKVLWRERAWFPPAI/MG IYYLDPSVLSGVSCFVMFLCLADY LVPILAPRIFGSNKWTTTEQQQRFHEI CSNLVKTRRA
1358	6855	A	1456	18	741	AACGAFSRVVVGVRVSVGGLVGEV ACACRDCIPETMAEGDNIRSTNLLA AETASLEEQLQGWGEMLMADKV LPWERAWVPPAIMGVVSLVFLIYY LDPSVLSGVSCFVMFLCLADYLVPI LAPRIFG\SNKWTTTEQQQRFHEICS NLVKTR\RAVGV\WKRLFTELKEEK PKMYFMTMIVSLAA/VLLAWGQQV HNLLTYLIVTSLLLPWT*TQHGIH FERTLGMANMEINKLLKHK**TN
1359	6856	A	1457	2	529	GRVDPKAKKEAPAPPKAEAKAKA LKA\RRKAVLKGVHS\HKKKKIPHV HPPF\RRPGRHLR\LRQPK\YPPEEP RPRRNKLDHYA\IKFPLTTESAMK KIE\DNNTLVF\IVGCLKPTKHQ\I*Q GC*RKLFWTLDVGAKVNTPGFGPD GRRRKAYVPTWLPDLPIAFGMFAN KIWGF
1360	6857	A	1459	323	624	IVVHLVPTTQRSGKGKIMELVERSV VARVEVGHRGFLERGLPIAINDM KKSPEIISGRMTFVQPRNWLLFACH ATNEVAQLIQGGRLIKHEMTKTASA
1361	6858	A	1460	438	549	
1362	6859	A	1461	210	556	QFWGPVATWGLPIDAINDMKKSPEI IQWGG*HFALC\CYS\LTFMEILPYK V\QPSGTWASCFAHGTEVRPSFI QGEGRIPNTRMDLKRASGINQWG KGKNKVFEGDSLCPGCC
1363	6860	C	1462	110	509	MLLICSFAPATLXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXVSA*
1364	6861	A	1463	93	180	
1365	6862	C	1464	128	382	MYLGISRRLLSSMLTFLAYLHPRERP PHRAPXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXQQAQG TGISIPRTCTSTGL*
1366	6863	A	1465	3	140	
1367	6864	A	1466	1	609	
1368	6865	B	1467	1	690	MASWDEKDLTVPQPDTRKGSVLR GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVGRSESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGVELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
1369	6866	B	1468	1	975	MSPPGREQGLLLNLLRPSGLDNAG KTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWWVDSADRQRMQDCQ RELQSLLEEVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRKSLACLLQL SSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNF CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH*
1370	6867	A	1469	25	353	EVCYYRSSEAFFSELIKVILRHLCSV AGKGLCSIPQLNTREGSVLRRISK GSPLAVEIEEGHCL\CLPLGTECLGI KPIVHLLNSEIGEKPPFSPSPSSA AFLLLR
1371	6868	A	1470	79	467	RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCL\ CLPLRTECLGIKPIVHLFSCTRPVIV PSLELHYDIDSIAHMFVADLLLIITLL SYYIPFYLGFQNA GITGINHRAWFY
1372	6869	A	1471	368	611	LCPSHFAPTTLTQSGSSLKTCVVLNS RFKACRAVPGPCLVNQMFASSILG\ KSHHSLVPINQGHNALWKAAGPL PLKAGY
1373	6870	A	1472	441	1178	FVALPQPLCPSHFDPTTLIQSGAHKN MCCIKSRFKRDLGLCRTCLVNKMF TSSILGKSHCHSLVSINQGHNA PWK AAG\PLPFRAGYC\QGFSPCDSLKYG \SWDEKDLTVPQPDTRKGSVLRWIS QRGKPLAVEMEEGHCL\CLPLGTEC LGIK\PPIVHLFNSEIGENRP\MVGG\ RHVLQ*CCLG*FL*LPLRCLG\GEKH KSGH/HVHIPVIVLS\LELNYDIDSFA

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						HMFF/SVDLLLIITLLSYIIFC
1374	6871	A	1473	1540	1812	GKFQLIKTLQNPVVCSLPVPALWG GQRWVDHLRLGVDRD*PGQHGETPS LLKNNNNNTKISWAWWHEPV\IPA\ MGEAEAGESLEP\GRRRLQ
1375	6872	A	1477	1	354	
1376	6873	A	1478	1	411	
1377	6874	A	1479	2	265	RMYGKIIFVLLLSGIRNVHPK*IVSIS ASSTTGVMHTSTSSSVTKSYISSQT NGITLINWWAM\ARVIFEVMLVVV GMILISYCIR
1378	6875	A	1480	111	520	
1379	6876	A	1481	106	395	EEALPPPLHCTWVPFSPFECLQEMS KEIVSISALSTTEVAMHTSTSSSVTK SYIS\SQTNGRKRDNLSDRFHCTSSC SDNTSLFLCVMGWYYWERS
1380	6877	A	1483	3	1078	TRAAGLRAGVRVPRSPGSPRRMPA RSGAQFCRRMGQKKQPARAGQP HSSSDAAQ\APAEQPHSSSNPAQAP CPRERCL\GPPTTPGPYR\SIYFSSPK GHLTRLGV\EFFDQPAVPLARAFLG QVLVRRLPN\GTELRGPHRWETEA/ YTLGPED\EAAPLQGGWPGKTPR\N RGMFH*KPGD/LWVYIYGYFC MNISSQGDGA\CVFLARALEAPGKS WRPMPRLRS\TLR\KGTRQARVLKG PPKLCSPG\SKL\CQALPINKSF*PEG TLAQDEAVWLERGPLEPSEPAVVG S/APRVGVGHAGEWARK\PLRFYV\ RGSPWASVVDRVAEQDTQACAKG LPRQDFLHCLKTRINVLFLEKKKKK
1381	6878	A	1484	3	452	
1382	6879	A	1485	26	493	NSTDSETHPWLLSPARQRPSTRPA WGKVGAAHVRSMCAEALERMFLS FPT\TKTYFPFHD\ASHGFCPG* RATG KKVDDSDAQTPWPTWDDMPKRR PP*SDLHAHKLS/RLDPV\NFKAPKA TCLAG*PLAAHLP\AEFQPLAVARLP WGQISWGFC
1383	6880	C	1486	30	200	MCISYTKGHFVVVWWVFPFGFSKILF RYISCPAPCRSSRMQSQCAHSSQSE VPGHRA*
1384	6881	A	1487	31	664	APALPGCEHMMMAIRELKVCLLGDT GVGKSSIVWRFVQDHFHDNISPTIG\ ASFMTKTVP CGNELHKFLIWDTAG QERFHSLAPMYRGSAAVIVYDF TEAGFHFHPLKKWV\KRLKELGPE\ NIVMAIAGNKCDSLDIRVPEPGL KEY\AESIGAIVVETSAKNAY*YRKS SFKEISRPDPHPWTPHENGNGTIKS *EANPCKPVRRC
1385	6882	A	1488	124	1180	DLGKPLFKVQEEGGRPPTLNQSEVV ALCPQPGGANHDARSLIMDSPRAG THQGPLDAKTEVGADRCTSTAYQE QRPQVEQDGKQAPLSPGLPAMGGP GPGPCKDPAGCGGAGA\GGSEPLVT VTVQCAFTVALRARRGADLSSLR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LLGQAFPHQ\AQLGQLSYLAPGEDG HWVPIPEEESLQRAWQDAAACPRG LQLQCRGAGGRPVLVYQVAPPFPK RGTPKPKRALDPFPPSPPPPPKGPE DLGFRQGD TVDVLCE\VGWAWPFP GSTVVPGVWGA*SSACAVSRRTGQ KATPG*PAEPDVPLAVDQAWLEG HCDGRIGIFPKCFVVPAGPRMSGAP GRLPRSQQGDQP
1386	6883	A	1489	1	229	
1387	6884	A	1490	3	461	AASTRFRASGQFVMAGAGSAAVSG AGTPV\AGPTGRDLF\AEGLLFLRP AVQQLDSHGHA VRESQVELRDQID NLATELCRIN*GQKVAL\DLDPYVK KA\ILNARRRV\VLVNNILQ\NAQE\R LRRVNHVR\VAREQPARRAMLDSGIY PPGSPGK
1388	6885	A	1491	1274	1416	FGIFSQFSVLH*SGK*A*NYYYYYY YYCYFYKMEYGSFFNLQVTF
1389	6886	A	1492	243	1125	FQQLRYRAARRFTMVKIAFNTPTA VQKEEARQDVEALLSRTVVRTQILT GKELRVCHPGKKEGSSGEMLWFTL FRAFQFILG\GLYLFGGACIYK/YTF MPKRHHFTVGEMCFFDSED PANFPF GGGEP*LSCLVT*/EEADIREDDNIAI IDVPVPSFS\SDSPAANYFMTFEKG MTA\YL\DLLLG\NC\YLMPLQYFYL LWPPKKIWVELFGQTGRVGRY\LP\ QTYVVR\EDLVAVSRKIRDVSNLGI FYQLCN\NRKSFRLLRRDLLGFNK RAIDKCWKIRHFPN\EFIVETKICQE
1390	6887	B	1493	28	282	MYHDWRLVPKHEEEAFTAFTPAPE DSLASVPYPPLLRAMIIAERQKNGD TSTEPM LN VQRIRMEPWDYPAKQ EDKGRAKGTPV*
1391	6888	A	1494	2	187	QNDRKMETQA/PEEPMLNVQRIRM EPWDYPAKQEDKGRAKGTPHPTPR AHAGESGKRS LPFH
1392	6889	A	1495	302	771	RKRGVCTHLLCRRRSASNCRAPALP SLTFEGQDAPGLPVVQVLRVVGVP HPREAPVARLVVLPQPGLARDQAA QAEEREAAEQ LQ/AGGSRGARRPRP GPAAGVQRTAASRSRSPRRAGSRA ACSVAPAGRARGGPAPRSAADAPS SAPWRVRVLSG
1393	6890	A	1496	497	1212	SWPGGEAGTARRPGCLPAPA*TR*R PPRAWAPAASHGT*RVRSPAPRSQ SSLMKKKRR\FEGQDAPGLPVVQV VQSHKQAGSARKALGPRGQEVGAS /DHANLQGGGEAGRPAGCRVGVRT GCTHLLRVVGPHPREAPVARLVVL PQPGLARDQAAQAEEREASEQLQQ SGSRGARRPRPGAAGVQRTAASRS RSPRRSGSRAACSVAPAGRARGGP APRSAADAPSSAPWRVRVLS
1394	6891	A	1497	852	1562	FGKAGWELNRRERGSWRVEEKDL QRWGVCGGGLCLPKPVRSGVCLS

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						LKHISGGLRRTLSQAPNWRNNSNGR VRGKHSNLNAQPFHPSLSYELKPCC VSQGLQRGILPPPQVSGPTFCSPKAL TPPSVRVLPPPPPP*CAVCMVNSP PALPTPLAKVSPADLAPRD*AHISG* RG*PLGHPHLSPLMLFTSPEPSE/PPP YPPSAP\PSSFSPARPAPPTVWPPPM QHRLWLPFPSS
1395	6892	C	1498	127	355	MKNRILQRNGXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX*
1396	6893	A	1499	529	2082	FLDLLHFTTSLIIPHYKRIRDLTYTIR HFPFVHLSPKCLDRPLSLFIHLGLV/ VIL*ALEPIH*SSSFLFH*LKIFSSPLW NI*VSPTFDSHF/CFLLILNLFLLSFPL SALI/NFQLQF*IKNETFHTLLIG*SEH *I/HT*MISTLFWLWK/LLLTGSLV*A RIFSCVHTQYHHACAIEKEMYLSSL FLFFMNNSKSCILFCIIIGPEFFDILL IC/LFFFLD*IIFSSIPALQ*YYLWALN AHSSQKARDSMLS/F*/ILVCWIAVT LG*DTLLAVTLE*DILSKVHCFMDPI SSSFLVFNPFGWENFPQRYFPQVR VQRRLS*KFA*QEKCPPLWMFLPEQ SALTMKFLGYQKISLKALKDVPID FWAFSVG**QIC*QSISHPFLC*ANR DDLICFLPGHFNIFLLSLIFQNFTILC LDVRLYWALSIWRLSL/RLFFN/IFFF LFLHLTSLASLPGTPNITY*MTMSL FFLY\FYYLSLFA\YLGEIPSTLFFQT VYQILLAVLFYFQRDLFYSQSSLSFP
1397	6894	A	1500	3	930	SSRGRAGGVWRFERDEDGTGAGCG QWTRFCREPKMAVNVYSTSVTSDN LSRHDMLA\WINESLQLN\LTKEQL CSGAAYCQFMDM\LPFGSIALKKVK FQAKLEH\EYIQNFKILQAGFK\RMG VDKIIPVDKLLKGK\FQDNFEFVQW VKKFFDANYDGKDYDPVA\AR\QG QETAVAPSLVAPALNPKKPLTSSS AAPQR\PISTQRTA\AAPKAG/PLGV VRKNPGVG\NGDDEAAELMQQGQR I*NLLFEDLGGKERDFYFGKLRNIEL ICQENEGENDPVLQRIVDILYATDE GFVILDEGGPQEEQEEY
1398	6895	A	1501	3	87	
1399	6896	A	1502	1	667	RRSSARRGGRSEPGRAGGGAAED TRRRAGDMRGEQGLLRTPVPPEE GEDVAATISATETLSEEEQEELRREL \AKVE\EEIQTLSASVKQKQRKHLA EIQAGNLGINSLQELKQNIAGGW*D VTVT\SA\YKKT\SETLS\QAGQKA\SA AFSSVGSVITKKLEDVKNFPNFLNH FEEKVENLKS\KVRGH/TKPAGGDF\ GEVLNSAANASATTTEPLPEKTQES L
1400	6897	A	1503	1	395	AKAKMADVLDLHEAGGEDFAMDE DGDESIHKLKEKAKKRKGRGFG/SR

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						*VWGKWGRVA**GRSYGFWSPHPP HRNNGRKEEFSVISCMSLIEEGSRA RMREDYDSVEHDGDEPGPQRSVEG WILFVTGVHEEA
1401	6898	A	1504	146	833	CLSGTDEISIEGEMADVLDLHEAGG EDFAMDEDGDESIHKLKEKAKKRK GRGFGSEEGSRARMREDYDSVEQD GDEPGPQRSVEGWILFVTGSP*RK PEEDIHDKFARIMGEIKNISSSTFDR RTG/YILKGYTSLNIETYKEAQA MEGLNG\QDLMGQLGGV\DWCFVR GPPK\GKRRGGRRRSR\SPDRRPSLT GPLLSRCSLQDSIWMAALGQIGLG WELCCVYI
1402	6899	A	1505	717	1563	APLPAVLTQTIHLVTGTAFHSGKVD IVTIGYPFIDLNDMVCMSQYDSTHG *FHSTVKTENGLVINGNCITHHPR RDPTKIK*DDAGTEYVVESTGVFMT MEKAEAHSAPSADG\LNDEKYENSL KIIGNASCATKGFAP/LPAKVIHDNF GIVEGLMAMVHAITATQKTVDGPS KK\WHD SHGALQNIIPASTGATK/A GMAFLVSTTNVLVMDLTLEGILGY TEHQVVASDFNSITHSSTFKAGVGI ALNNHFVKLISWYENEFGYSNRVV DLMVHMASKGSS
1403	6900	A	1506	625	2919	
1404	6901	A	1507	2	76	HHYAKLGTRAVRRARRCAGWQSY VDNLMCDGCCQEA A IAGYCDAY VWAATAGGV\FQSITPIEIDMIVGKD \RKGFF\TSGTLGA\KKCSVIRDSLY \VDGDCTMDIRDKQS/QGGEPT\YNV A\VGRSGRALVIVMGKGVFHR HTLTRKAYETPLYT*RQAWHEGSA KGSKMCR LAELRG
1405	6902	A	1509	63	290	GGILLSISRPHYKTKPTHGIGKYKHLI KAEEP\KKKKGKVAVRAINLGTDY NYGV LNIH\LTAYDMTLAESYAQY VHN
1406	6903	A	1510	315	1092	RPRSSKRMSGTSEKVLCLRNNTIFK QAFSLLRFRTSGEKPIYSVGGILLSIS RPYKSK\PTHGIGKYKHLIKAEEP KKGKVE\RAINLGTDEYEGVLNI HLTAYDMTLAESYAPLFSTTFCHNSL SH*KSEESYAMPTQNHKKWLPVCR DQGQPKCLLGLKCLPHERV\VOIS GLSATFARKFSWKIIPKPVLP*RESG LFS*REHTERKTSRGRFQRFDP ELGRTFWAKFEVATVDPFHCQQWSYLSA KEKSLG
1407	6904	A	1511	284	758	KQNPSSPLQRLIAGSNLDSEPRIQTD ILKQATKDRVSDFHKLKQSRFFDEN ESPVDPPQHSGSKLADYNGDDGNVGE YEADKQAE LAYNEEEDGDGGEEDV PPDEEREL/PNGKKQAMESNISMMS FKS*RNA SENLKCKMKSFYFVLS D FCKDELYQL
1408	6905	A	1512	148	476	

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1409	6906	A	1513	204	620	GDAMAAVTTPRPPLPEGCRAPSSAPT VSLPELRSLLASGRARLFDVRSREE AAAGTIPGALNIPVSELESALQM/DQ LAFQGFIFLLEKPKLGR*ASSFSFLFR WGKRGLQATQLARSLGYTGGFATY AGAY*EWLEKES
1410	6907	A	1514	1386	1711	FPKSIMGLVTIQDMNLCKIFIGLSHL PALVLLYC/DVRACVMSGC/LRKTS EKNLKSRRPSFFACSILSRNVQCNWT KIGMFKDI*GFFCFPYFYLFVSCIFA YLCRFSGF
1411	6908	A	1515	481	1380	TSKQNAAPLVKYFQEKGLIMTFDA DRDEDEVFYDISMAVDNKLFPNKE AAAGSSDLDPMSMILDTGEIHDGSDY EDQGDDQLNVFGEDTMGGFMEDL RKCKIIFIIGGPGSGKGTQCEKLVEK YGFTHLSTGELLREELAS*SERSKLI KDIMERGDLVPSGIVLELLKEAMVG \SLGDRGFLID\GYPRE\VKQGEEF\ GRRIWRPHSWVICME\CSADTMTN RL\LQRSRSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETK\QLHKINAE GTPEDVFLQLCTS*LTLFSEGKNA CLG
1412	6909	A	1516	47	416	NSYIYMCISYINTIYIHIYLESNISLP LNIYISTPT/HIY*RHTV*VHTKAYV HML*HVYIHFCLCVHKSFKGTIYRD ASFLESCSKVNTECHKLRKVKRKYS RIHHTGIHQSSLIITSPFTF
1413	6910	A	1520	1386	1666	SLMAPQKMGRITSCSPSERLGN*GPE TGSDSHKTPQQGCKGGRTRGSIVSL GDRRPLAP/GACFAGDKDFLGLRSP GVGTALLGCTINQRLWA
1414	6911	A	1521	304	1253	VTNEMSQGVGKYDFYIGLGLAMSS SIFIGGSFILKKKGLLRLARKGSMRA GQGGHAYLKEWLWWAGLLSMGA GEVANFA\AYAFAPANSSGLHLGAL \SVLVKCPFFLSYFLNERLNLHGKIG CLLSILGSIVMVIHAPKEEEIETLNE MSHKLGDPGFVVFATLVVIVALILIF VVGPRHGQTNILVYITICSVIGAFSV SCVKGLGIAIKELF\EGSLCCGIPWA WILLLSLIVCVSTQINYNRALDIFN TSIVTPIYYVFFTTSVLTCSAILFKGV GKDMPPVGRCPVL*SGFFTHVGGY SCCMPLKTSALA
1415	6912	A	1522	20	131	KEILPKQAFVAVPTYITEPVEIKFFFF SRIRL*VPPG
1416	6913	C	1523	7	348	MSKLYIMQFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX TV*
1417	6914	A	1524	1103	1388	VLLIFNLFPMALYFVCFSE/CFFETEA HSVT*ARVQWHDLGSLQPLPP*FK* FSCFSLPCS*YYRHLPPYANFCIFSR DGVSPCCPGWS*TPNLR

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1418	6915	A	1525	149	421	
1419	6916	A	1526	1	1107	
1420	6917	A	1527	25	1486	GPQQPHSRSTHASGRPQSLSPVLSLS PDSMSFTTRSTFSTNYRSLGVSQAPS YGARPVSSAASVYAGAGGSGSRISA SRSTSFRGGMGSGGLATGV\AGG\L AGMGGIQNEKETMQSLNDRLASYL DRVRSLETENRRL\ESKIRE\HLEKK GPQ\VRDWSHYFK\NEDL\RAQIFA NTCGTMPRIRSARIDNA\RLA\ADDF\ RVKYEDRSWPMCPVLWRTDIHGLP KVH\IDDTNYHTDLQLETENEALKIE ELLFQ*RRNHEEGS*KALRRQ\SSS GMNAWRLD\APKSQDLAK\IMADIR \AQ\YDELGSKKNPRGSLDKY\WSQ Q\EESTTGGSPQKSAEVG\AVETHA HRSLKRTVPVLGRSTLDSMRNLKG QLWRTSLREG*RPAYALTRLEPAPT GSL\HLESEL\AQTRARGTAARPRE YEALLN\IK\VKLEAEIATYRRL\LED GEDFNLGDALDSSNSMQTIQKTTTR RIVDGKVVSETNDTKVLRH
1421	6918	A	1530	277	693	PWHCPDSHYSQQPGSTASSSVPART GGPCWSSSCSPN*CTSCCSTTPTPT LDPR/GSRHCQLPWLKQLPKGM/CT STCLHGSCGCICGSCGPGCIDGPTL GRNHNEPHHHSHGDLPYRFPEHAH HGHATLMGLMDTPLV
1422	6919	A	1531	1	364	PFVSLGLMCFGALIGLCACICRSLYP TIATGILHLLADTML*SPGHMEVSC VDAPAEIPS*APN*QPTSFPAMCGSH PGCPALTSLQRTSATAILLHPCETLI KNQLAEPNQPMELIEIK
1423	6920	A	1532	1	898	RGESRVLWSELEGEAGGAGGWASS LNARMDNRFATAFVIACVLSLISTIY MEG\SIGTDFWYEYRSPGQENSSDL NKSIWDEFISDEADDATYN\DALF\R YNGTVGFLRRVYSPYPKTLHWVLA HHERTESFDVVTK\CVSFTL\TEQFM EKF\VDPGK\HTNSRGLDLLRTYL\W RCQFLLPF\VSLGFDVLWGALIGLC A\CICRSLYPTIATGILHLLAGLCTLG SVSCYVAGIELLHQKLELPDVSIGE FG\WSFCLACVSAP*QF/LWASALFI WAAHTNRKE\YTLMK\AYRVGMSK KPACF
1424	6921	A	1533	939	1591	LQSLCRVLLQMESGSRDITPGVCKR ERENREDTEVLQPRFPYQGGQLVG KAATPQPFG*STVGWTLQPQ*P*YP AGQGCPP\RCPPAPSS*GSKRPPEPQ QGRLGPKPGSPQA*GNASPPKCPA PVPTPC\PPTLCTGEKTGGARAGPW VGAGSPW*DPR*DGPIPCVGDPLSP HPCCVIVALLPFNVSVPGGRGGAPP QPP*T*PKAMAVAPPFV
1425	6922	A	1534	34	912	GRIRMQRQSTTGGRGIMEGPRGWL VLSVLAISLASMTEDLCRAPDGKK GEAGRPGRRGRPGLKGEQGEPGAP

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						GIRTGIQGL\KGDQGEPPSGNPGK VGYPGPSGLGARGIPGKGTKGSP GNIK\DQPRPAFSAIR\RNPPMGG\NV V\FDTV\TNQEEPVQDPSG\RLVCP EPGYYYFT\FQGAGPQWEICLSIVSL LQGARVRRSPGAF*HPPTRGLFQV VSGGMGL\QLQQGDQ\WVVEKKPP QKGSIFYQGE\ADS\VFTGFL\IFPIC LSQGRTPSPPTSLASMLRL
1426	6923	A	1535	919	1260	YSVSEFRGQTLTAKFCFFERESHV PRLECRGTILAHCNLCPLGSSDSPAS ASRVAG\TTGACHNARLIFVFLVET GFHHVVQAGLNS*PQVIHPPCPPKV LGLQACTWHLAH
1427	6924	C	1536	130	441	MVQNKGQLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1428	6925	C	1537	5	316	MVQNKGQLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1429	6926	C	1538	74	91	MTLAM*
1430	6927	A	1539	368	430	
1431	6928	C	1540	191	592	MGQQPGQARAPSYCRCPLSPGSGR ALRWERPGGGQGPKEIVLSGCVPE KGPQTPAQPHSLRHLQNPEATARTG EEATSAAGGPWASPSFGGTQLCSDT MPALLGARSTCWIATHVCTPLS ECGPINILLE*
1432	6929	A	1541	58	1531	VIAVTSALPGRTQAAWTRVVKMDL LAAKMAVGGGSLMTDLTSSISKPL VPVGNKPLIWYPLNLLERVGFEEVI VVTTRDVQKALCAEFKMKMKPDIV CIS\DDADMGTADSLRYIYPKLKT VLVLSCDLITDVALHEVVDLFRAYD ASLAMLMRKGQDSIEVPVGQKGKK KAVEQRDFIGVDSTGKRLLFMANE ADLDEELVIKGSILQKHPRIRFHTGL VDAHLYCLKKYIVDFLMENG\SITSI RSEL\IPYLV/RGKQFSSASSQQGTRK EKEGGSKGKRGKLSFRISYSFY*KE ANYTGTGAPY\DAC*NACRGDRWE DLSRSQVRCYVHIMKEGLCSRSTL GLYMEANRQ\VPKFLSALCPGRTHQ SISSSPDCQHYTWVGVD\SLIGPRDH RLGEKVIPLSASVIGSSL/CLIKDRVT ITNCL\LMNSVTFWRKEANIQGSVI L\NNAV\IEKGADIK\DCIIGKWARRI EA\KAKRSVCR*S*GNDQLMEI
1433	6930	A	1542	315	644	EEETPKDQCLGAHFSSDTFPRQSRL LGVHGRGAGSLCTGLLSEHCPSTPP SGSPRV\TYLPH\PPLPSP/SWAPTP PAHR*KPSTEPFPGPSTQVV*PLPMF TTKGAPP

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1434	6931	A	1545	1	364	FFFFF*DGVSLWPRLERNGVISAHC NLCLPASNDSPASASLVAGITSAC/R PLPPKQK*LFFFLRWSLALSPGWSA VARSWLNATSPGYF**KQGFHHAG QDGLGLLIHPPWPPEVLGLQA
1435	6932	A	1546	1	391	
1436	6933	A	1547	2	2371	GPPGRARARGLRRAPAAFLRRSLSL PAAFSSAAGPSSPQRSQEGRRPREPTP RSSRGSRGSRPRRLRLRRGRSAIH GEGRTAKGSAAWSARTFRSPPGVG RDPMRRRAHEGREIPSLGGARRREVL QAGRSQRAAGRRRRRQEELELVGS GRPGGPPPGPGRRGTCAAALPPEWP RRRTGLPRRGPRPPLAMAKWLNKY FSLGNSKTKSPQP\PRPDYREQRRR GERPSQPPQAV\QASSA\ASASCGP ATASCFSASSGSLPDDSGSTSDLIRA YRAQKERHFQDPYNGPGSSLRKLR AMCRLDYCGGSGEPGGVQRAFSAS SASGAAGCCASSGAGAAASSSSSS GSPHLYRSSERRPATPAEVRYISPK HRLIKVESAAGGGAGDPLGGACAG GRTWSPTACGG*KLLNKCSSSSAEE SGAGMKDKVTIADDYLDPFDAKND LKSISGKGESAGYMEPYEEQIMTE Y*RQECVRSQH*GIQLYETP*EPEGQ NFESESESTVNPRMRENKLPQDYEQ /RPAD*Y\DQPLELNPV/TQFPALAA QFNGNEKPQSSPSPSR\DRRRQLARA PGGGFKPIKHGSPEFCGILGERVDP AVPL\EKQIWHYHGAISRGDAEN/LCL RLCKECSYLVRNSQTSKHDYPLSLR SNQGFMMHMKLAKTKEKYVLGQKS PP\FDSVPEVIHYTT\RKLP\IKGAE HLSLLYPVAVRTLLSGPDSALLCDR AWRLARCQRPTNQPATVAGCVV CVVCMVLAHHCMSLECCCHLRGLE KAWIKTEGRQHTTSPNPNEALEFL
1437	6934	A	1548	304	678	PQVILPPLVSQGCWELPDVSPLRPSL VW*FL/RK*KLDLPCDPAIPLLGVIYP RKIKACFHTKTCIQIFIATLFGIAKKK GKQPKQPSAGEWINTW/HIHTMK HCSAVKKEQTETISLFRSRIWRI
1438	6935	A	1549	80	623	LGGVTRGFNMRIEKCFCSGPIYPG HGMMFVRNDCKVFRFCKSKCHKN FKKKRNP\RKVRWTKAFRKAAGKE LTVDNSFEFEKRRK*TYSNYQRDLL GIKTIDAMKRVEEIKQKPPS*IYNEQ IE/GKIKSYRKFDIKRSPSQNIPSL RAPPCQAKGKQLGEEMGTARLQGG CGHGKMPP
1439	6936	A	1550	1021	1544	EPTKKCCVYYAQFLSLPSLFFPTGSE EQDSIYFILFFEMEFRS\VTQAGVQW CDLGSLLQPPPGFKRFSCSLPSSWD NRLLPQGPANFCIFSR/GWGFHRVG QAGLFSRDGVSPS*SGWSRTPDLVI RPPWPVRVLECSGQYIIFPWLFSRFS LSIFSKFDCNLSQFGFIWICLFYSS

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1440	6937	A	1551	2	210	
1441	6938	A	1552	2	310	IGVKMEEYAREPCPWRIVDDCGGA FTMGTI\GGGIFQAIKGFRNSPVGVN HRLRGS\TAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWNSI TSGCLNGEPYWQARNGTQWPMVG VSPQWVGIFPSF*FEGSWYLCLTRF ASGTVFPMGP\QFA\EDPSPVCLSTQ LPSL\PFGGGIFQAIKGFRNSPVGVN HRLRGS\TAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWELH HKWVP
1442	6939	A	1553	1	4629	
1443	6940	A	1554	96	721	PGQLSSLTPPRPASLLPWRAAYLFL\ LFLPAGLLAQGGYDLDPLPPFPDHG QYTHYMDQIDNPYYDYQEGTPR\ PSEGQFQ\F\QSQQEVQQGVIPSPNPR AQGNAEL\EPTEPGPLDCREEQYPC\ TRL\YSIHRPCK\QCLNEVCFYSLRR VYVINKEICV\RTVC\AHE\ELLRA\D LCSGTSFSKCGR*WASSGL\CQSV\A ASCA\RSCGSF
1444	6941	A	1555	262	732	FQNKGNFFSTKRTEVSPSTQFNFYFA RKNTTLIRISHSSLGQVRIRLVWFG LVWFWFLETGV\CTLVIRGWEFQW\ CDQNSLQP*TPGLQRIFPTSASQSTG ITGVSHSLVRYVVFVTEIQLKFWILI TKITVLLVYN*L*NKGY*YIFITFFL NLQN
1445	6942	A	1556	162	496	HSYIHIVHVCNFFMYSFAVFVFKKH LLLCLYNRTVIIYYNLGKL*INS*FK QPVYMHI*VLYC\INLCFTYMKAA RILLICNYTHKIYICMIHEIYLEMFII LMDILWCE
1446	6943	A	1557	2	247	GEIVVFKVEGRDIPVHRVIKVHEKD NGDIKFLTKGDNNEVDDRGLYKEG QNWLEKKDVGGRAR\GYALLAVM GAYVLLKRES
1447	6944	A	1558	1	503	VRAGAVGAHLPASGLDIFGDLKKM NKRQLYYQVLTAMIVSSALMIWK GLIVLTGSESPIVVVLSGSMEPAFHR GDLLFLT NFREDPIRA\GDNGDIKFL TKGDNNEVDDRGLSKEGQNWLEK KD\VVGRRARGFLPYVGMVTIIMND YPKFYALLAVMGAYVLLKRES
1448	6945	A	1559	180	257	
1449	6946	A	1560	2	676	FVRCSAAVCATQSRRAARSPENPA MVRAGPPWGLNLPASRLGISSAD\L KKMNKRQLYYQSFKPSPWIVSSAL MIWKGLIVLTGSESPIVVVLSGSME PAFHRGDL\LFLT NF\REDP\IRAGEIV VFKV*RPRTFPISQR*SKVHEKD\N GDIKFLDLKGDNN*SLMD*EALYK KARNWLEKKDVGGRARGFLPYVG MVTIKMNDYPKFYALLAVMGA\ YVFLKR
1450	6947	C	1561	449	820	MVIXGQISPMATSGQKAFLAGPLG

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						SLGTLPRSQA VKRRLLKLT KDRI RDVLLMFLKGHRETHGQCLQRQQ TKESTSIVVLALCGLYGKQVVTLLN VGIPFSIN VYFTTPKSPLIMKLI*
1451	6948	A	1562	251	473	
1452	6949	A	1563	22	212	
1453	6950	A	1564	160	397	
1454	6951	A	1565	17	262	LFWAKALNRHFSKKHIQMANQH MKRCSTSSAIREIQVKIAMVYN*YTI *HSQ\YSLQLPFPLWKT VVKFLT VV KLLNCSVK
1455	6952	A	1566	2	294	GNKMAAPKGS LWVRTQLGLPPLL LTMALAGGSG\TASAEAFDSVLGDT ASCHRA CQLTYPLHTY PKVGPVRS GLRPFPCSPFLGSPHVCRLWQPGC
1456	6953	A	1567	366	1412	QRGTRWRRERGS LWVRTQLGLPPL LLTMALAGGSGTASAEAFDSVLG DTASCHRA CQLTYPLHTY PKEEEL YACQRG CRLFSICQFVDD\GIDLTRT KLECESACTE\AYSQSDEQYALPFL GCQNSACHFAE\LRQEQLYVPRWP KMAPTFFL*LLGEGSFWELT*WDSA Q\SFITSSWTFYLQA\DDGKIVIFPV* SQKSQYAPHFGAREPTNFEENHLLS KMSSDLQMGKFHQAHQGIFLKNEE RDGLFKKPSILNSGWILTTTLVLSV MVLLWICCATVATAVEQYVPSGE AGVTMGDLEFMNEQKLNRYPASF SCGLVRSKTE\DH EEA GPSYLPKVN LAPFLEI
1457	6954	B	1568	76	384	MSGWGVLSGR LNPAAREKDVERFF KGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELC SERVTIEHAR ARSRGGRGRGRYSDRFSSRRPRND RRNAPP*
1458	6955	A	1569	3	229	
1459	6956	A	1570	152	536	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDP K\ADDAVYELDGKELC SERVTIEH ARARSRGGRGRGRYSDRFSSRRPR NDRRNAPPVRTENRLIVENLSSRV WQVC
1460	6957	A	1571	771	1383	ILIEYKCGKCHVCTLSNIFSFSSLVFF ISCDCLCVFPPLLCTQLSCVKDLK DFMRPAGE\VTFA\DAHRPKLNEG VEFASYGDLKNAIEKLASEKEINGRK IKLIEGSKRHSR SRSRSRTRSSRS RSR SRSS\KSYSR SRSRSRSR DVPVLLSRSPRA*EEPRNRGSSSRK SPASVDRQSR SRSRSRVDSGN
1461	6958	A	1572	236	1377	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELC SERVTIEHA RARSRGGRGRGRYSDRFSSRRPRN DR/RVCEGWMAALNNYW*G*PFKI QESLAVMILGPAV*SVLLFPR*PIVL DESI*VIEHKSIDGSH*NL*YLMA*

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						TCPQLNTSAVIAFLPL*IRIFFLRNAP PVRTENRLIVENLSSRVSWQDLKDF MRQAGEVTFADAHKPKLNEG VVEF ASYGDLKNAIEKLSGKEINGRKIKLI EGSKRHRSR SR SR SR TR SSSR SR SR RSR SR KSY SR SR SR SR SR SR SK SR SV SRSSPCPEKS\QKRGSS\SR\SKSPSHL WNRPEVPGPRSR SQIQLDQWPIKPV K
1462	6959	A	1573	568	770	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCS\ERV TIEHA RARFTRLGRGRGRYSDRFNNSAEL RNDRRNAPPVRP\ENRLIVENLSSRV SWQDLKDF\MRQAGE\VTLPD TTRL NL\NEG VVEFASMGDLRNAIEKLSG RELNGRKIKLIERPAKRPQ*VQQSR SDPGTQKSPLGPRSRSPSPV ANLN SRSKK\RRGSREPGSPEPSRSC*VGS SPVP*ERFFKGYGRIRDIDLKRGFGF VEFEDPRDADDAVYELDGKELCS
1463	6960	A	1574	22	202	TKSSS*CDSVATCGIIFSCPHNLSKI HDSISPRVC\SICKPHGSIHKLCIKIF HIFAR
1464	6961	A	1575	1	1878	MQYSHHCEHLLERLNKQREAGFLC DCTIVIGEFQFKAHRNVLASFSEYFG AIYRSTSENNVFLDQSQVKADGFQK LLEFIYTGTLNLD SWNVKEIHQAAD YLKVEEVVTKCKIKMEDFAFIANPS STEISSITGNIELNQQTCLLTLRDYN NREKSEVSTD LIQANPKQGALAKKS SQT KKKKKAFNSPKTGQNKTVQYP SDILENASVELFLDANKLPTPVVEQ VAQINDNSELELTAVVENTFPAQDI VHTVTVKRKRKGSQPN CALKEHSM SNIASVKSPYEAENS GEELDQRYSK AKPMCNTCGKVFSEASSLRHMRI HKG VKPYVCHLCGKAF\TQC NQLE NACKELHTGEKPYKCGICVIKGFAQ KC\QLVFH SRMHGEEKPYKCDVC NLQFATSSNLKIHARKHSGEKPYVC DRCG\QRFAQASTLT YHVRR\HYW EEKPYV\CDTCG\KAFVLLVLFHIS FLRK\HTGEKPYICGICGKSFSSGEL NKHFRSHTGERPFICELCGNSYADI KNLKKHKTKVHS\GADKTPRTPSA\ EDPNLG VKQDP\IQKSPFN PETYGCE SPS*YELYPLALPLGTED\HHMLLPV TDTQSPTS DTLRSTVNGYSEPLIF LQQLY
1465	6962	A	1576	42	134	
1466	6963	A	1577	154	768	HVACGLLWIYVSPSAHLNLDGTITT K/ENLGTVNEILLGSNPTEAELQDMI NEVMSDGNGTIDFP\EFLTMMARK MK\DTDSE/EKEIRRKHSRVFGLRVG NGLYLVACRNFRHV\MTNLGRKF NQIEEV*WN*SRGSQILDG*WSKLT YEEFVQMMTAKVRPLSRNVNLFLV

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						QNCFICLFLWFVTLSCKKVFSPTCQ KKNMHVIGN
1467	6964	A	1578	3	202	RRMVSAFSCRCMPSEPCIAVTAPCM MAGQAPAERTAQ*PLYF/CTLFQGS LSPT*REVGWPLGPAGM
1468	6965	A	1579	133	378	
1469	6966	A	1580	891	1744	DMFPITPSRSVLPSFLLTYLPRQSL/N SVAQAGVHWCDSLSSLPQPPPGFKQ FSCLSLPSTW*LGLQACTTVPS*FFV VVVCIFFFFLVETGF/TLGWARLVLN L*LQ/CDPPTWASQSAG/ITDVSHHA QPILRFKCLS*CIRSFNEGRIKGTRQ NKVELSL/CFLRQESHSVTQAGVQW CNLSSLQPLPPGFKQFSLTGLPKC WDYRSKRPRPANQTSILGC*RKDPY *LHWAKKATEDIKLESCRLTPGKAR PTANFLRQGQFFWGPILGGLLPQE GFPFLFFKGF
1470	6967	A	1581	2119	2436	TTRYLKKTSTTGQRKKRGRGNGSF PTENLVPSGTVTGSQQLGPPFR*N/H TEECWGPPTADGRAGKGPRQPGGR AQRIYRWDPDGTWVHHHRPCGSR GTDQPETK
1471	6968	A	1582	208	296	
1472	6969	A	1583	185	947	SHCSSGMEIPVDQLPSLPRAALVAQ NYINYQQGTPHRVFEVQKVKQSQA WKD\PGKEGHKYS/HLKFAV*KKL YKKQVKG*TCTA\EVLLPFQRGQET LHQEVNFHILKEKLGKNPD\EEDNT F\YQRLKSMKEPLQAQNA\PD\NFGN VSQEMTLVLNLAWVACGLI**WQK FLLKTTWYK\MVKI\QTCQARCQRI DDFIELDYPPFYFINIASQE\IPWQM QVLWHPQYGTKVKHNSRLPKEVHL GYTPKPLTLEV
1473	6970	A	1584	5060	5662	ESQAAPPPRSTLHRPARATAITAC WSSQASGPQAVRRLLTPLSSPAAR DLVSKEGFRRARHVGEIRRTAQA AAALRRGDYRAFGRMLVESHRSLR *GPLGAPLLPGTGRPRPTPSISLQ/D DYEVSCELDQLVEAALAVPGVYG SRMTGGGFGGCTVTLEASAAPHA MRHIQEHYGGTATFYLSQAADGAK VLCL
1474	6971	A	1585	2	987	LREGCPQR*RQPTQLDWPYF/CPFSP VC*KTKTKKPYPCAPKLGHVRCPT ASTLQAHTGPCPPSPQTGPQTRAGL LHICVGVGARFLFLLSLSPFGDIPL
1475	6972	A	1586	318	382	
1476	6973	B	1587	106	293	MAGRVCLCQGSAGSGAIGPVEAAI RTKLEEALSPEVLELSFRGTEPPTTT PAGPRSAGRAGS*
1477	6974	A	1588	442	905	PMLSGRLVLGLVSMAGRVCLCQGS AGSGAIGPVEAAIRTKLEEALSPEV LELRNESGGHAVPAWAVRLHFRVG CW*ALVFEGLSPLTTDTGLFHAALA EELGRFRSHALAI\PGTDPPPQWREN

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						\SQLEQLAPPCLG\GKQENFLGTPLE PPKRG
1478	6975	A	1589	1206	1335	KTQERYFNLKQN*TGQAWWLMH/I WEAEAKGSLEPRSLRPAWAT
1479	6976	A	1590	136	837	PSEKTSPPDRDKKKRAVRSILFLELQ NIIQDHDQGOEKENESQIMKEENT GAGAEAKREEDMNPVKSSKKHKS EEHNDKEHSSDKGRERLNSSENGE/ AQAQTPRKEGH/RKGRGHSRSRSRE RRHRIRGRERKKSRSSRSRERKKSR SRERKKSRSSRSRERKRIRSRSSR IQRHRA*D*KAGVGPRSSRDRKKR IEKPRRFSRKFKPDSQVHLPLEGRTO PWDQAQAFS
1480	6977	A	1591	209	1545	PYYFLQANSPPGPLLTPALLPHRILS DVTQGLPHAHSACLEKLKRSYEFY RYFETQHQSV\QCLSKTQQKSREL NNVHTAVR/SLWQLHLKALLNEVII LEDELEKLGCTKETQELVSEAYPILE QCLK\LIQPHVQASNNCWEEAISQV DKLLRR\NTDKKG\KPEIAC*KPTCY SSTF*RQPTLHIADQDPIEEQE\LEA YVDDIDIDSAFQNRHDFYYLSQEDK ERQKREHEESKRVLQELKSVLGFK ASEAERQKW\KQLLFSG\HVLK\SL FVGPQWEPISNSEPSMNSDMGKVS KNDTEESNKSATTDNEISRTEYLC ENSLEGKNKDNSSNEVFPQGAEER MCYQCESEDEPQSKIGSGLTTAPPT P\RDLSLQPSIKQRLAARLQ\SPDFTFT AGPCWQEVGCLDLLPFTTMAGNR LFGDEEEEEEQIIEEN\KNEIEEK
1481	6978	A	1592	1	296	DFPLPTLLKTGPGPGF/YNGPP*GER FYVASPG*IWAPQGFF*KGPPSSSSS SSSQRSKPLPFCFANKTG*VGCFLVI SQRDQIPYPRPTPPTLPWLQP
1482	6979	C	1593	15	350	MLISLNINQTLTYCNKTENCXXXXX XXXXXXXXGGPFKRTPGGPKFNRG WQKIFPLKGGLLKPHWGIFFXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXEKGEKQPEKPGG*
1483	6980	A	1594	11	129	APWLSVLY*SESPEAQPPYMMGPLE SP*AQRCPGLERGR
1484	6981	A	1595	2	660	NFPTARLFRLFYPLFLKIFIPKAFN FCREVGPFCPPPK*GFFPKIPK*VFN RPP/SKGSFTLPAPVKFGPPRGPFK RAPSSSSSSSPVV*APWPTVLY*SE SPEAQPPYMMGPLES*APHEGVTA WVES*GPCPA*PWGRQAAPQPPPP QERAG*EPESKFGPGSK/PPERPVYA GNSPVLRSGLTSPSPAPPGGFKY MEERSKADLGPGMEKG
1485	6982	A	1597	1	680	ESRIRRRSSRRPREPPGPSRRRRRRR PDPRTMPSEKTFKQRTFEQRVEDV RL\REQHPTQIPR**LERSKGNNQPP \VLDK\TKF\LPDHDVNMSELIR\IR RRLQ\LNANQAFFLLVNGHSMVS VSPHP\SEVYE\SEKDE\DGF\LYMV

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						LCPPPE/YGLR*TLNV*N*KKKNAAS S*NCLNPLPKEKIKECYPTIDQFIPI TDHETSSVPTLGLVGLSCVCVSSRKT
1486	6983	A	1598	2	508	PDSSGPHRLRENPPMVAVSCPTKTN VKGPPGGKVGAGAHAG\EYG\SEALE\R MFLSFPTTKTYFPHFDLASHGLCPR LKGHG\KKVADALT\NAVAHVDD MPNGVVVRP*SDLH\AHKL\RVDPVN FKLLSH\CLLVTLA\AHLPA\AEF\TPA VPRPPWDKFPWLSVKHRCLTFKYR
1487	6984	A	1599	295	758	VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTGMPQHVTQQ*RPIINTS HQYSVKLGHPD\TLN\QGFEKELVR\ KDLQNFLKKENKNEKVIEHIMRGP GTQNAQAELSRFIMLMGEA*PG AFPRRKIARGLTEGPGHPNK*PGPG GGAPP
1488	6985	A	1600	411	1259	SQGTTSRGSWEFPHSPEIEETSCLAE LFEKAAAHLLQGLIQVAKQGATLCT LYAKYKQVKVGNCNTPKPSFFDFE GKQKWEAWKALGDSSPH\QAMQE YIAVVIKLDPGW/ISSDIQRRNGKEA NTGFGGPVISSLYHEETIREEDKNIF DYCRGKQH*PYNQKPSNPKNVDVN VKDEEGRAP\LHWGL*SEDIKELVH SVAANIELTLNCQD\NERPKQALHY ASACGVSGIL*ELAAPSLGADPDSPR PGWLPARGGDRLQNSFFGAAAAHN WQGLIKRLENCSL
1489	6986	A	1601	177	409	FLQASGILKGFEPNLL\NLVLTVTI*Y MRDPDDQYKLTGGHPGKGLVVF G\TSLVL\ICPDGMEAI\NPFIQQQ DA
1490	6987	A	1602	1	165	PLKRSDGCNDGRPTRPPTRPDITVF TSNLKQTRMVHLTPVE\KSAVTAL WGKVNVDV\VGKALGRLLVLP WDPKRSFQSPLGESVPTP*MVHLTP VERVCRYCPVGQGERG
1491	6988	A	1603	240	461	
1492	6989	A	1604	2	206	
1493	6990	A	1605	2940	3296	
1494	6991	A	1606	189	736	ENKISSVFKADFLPPAPCSLPGLEVS VSPKGNKTSGRESFGWAIWMEGL VFSRLSPEYYELA\RPHLRDEEKS\CP C\LAQE\GPQG\DLLTKTPELGP*ITR TC\LTIVQKT*RKMDVKPTQRSVS NAATRVCTGRSRWRDVCNRFMR RYQSRVTQGLV\AG\ELAQQNLVST SRLCIPSTGPL
1495	6992	A	1607	3	452	
1496	6993	A	1608	3	485	PTLLVPTDSERTHPWLLSPADK\TN VKGPPGGKVGAGHAVRSMCAEAL RMFLSFPTTKTYFPHF\DLSHG\SAQ V*GPRARKVADALT\NAVA\HVGR LPNALVPPLSDLHAHKL\RVGPGSTF KLLKATCLAGLTL\AAHLPARVQPL AVASLPWDKVSWSAC

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1497	6994	A	1612	77	636	QPQTDTMVHLTPVEKSAVTALWG\KVNLDENVGGKALGRLL\VV\YPWD POKVL*NPLGESVPTP*MLVKWGKP PKGEKAQWQKKKCSGAL*VNGPGL T/HGQPSKGTFGPH*SELHC\DKLH\ VDP\ENFRLPGQQLVCVAGPITLG KEFTP\QLQACLFRKLVA\GVANAL GPTSNHLSLAFLAGPISN
1498	6995	C	1613	167	391	MNVFMCRLGTTFFHLVLLLPVLP SL RKT VFLNPFSIKQRFQRWKHWVFQ VASELTDAILSSCGHLFLPGSHNLS*
1499	6996	A	1614	1402	1871	GLQGSQSLHPSLTGLRHACITLGKT AHSSRLHSPAPPPYL*STDTRDNN APEPTPPRSWTWRA*/PMGRGSSQE GQASQQPWPGEKSGCEMPPLVY KVKPEP*P/SPDPWGL*QSMPLDYL HLSVILRWRRGGGQWQGATKISRR DRRGGALLHL
1500	6997	A	1615	8	551	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPVEKSAVTALWG KVNVDENVGGEDLS\RLLPVYPWTQ TFFD\SFADQSTPDAAMGNPKVKAH S\KKVLG\AFSGGPGCTWDNLKGT F AHTEVSLHC*QACTWDP\ENFRLLG\ NVLVCCCWAHSLLGKEFQPHQLQA CLIKKIGWLGVG
1501	6998	A	1616	3	389	
1502	6999	A	1617	1	672	
1503	7000	A	1618	18	621	RSLRCSRHSCLATSSPLPCARRAWH PARGKADQPFCSRAGSPVAAQPR GENREKEETTRIGPGVMESKEKRAV NSLSMENANQENEEKEQVANKGEP LALPLDAGEYCVPRGNRR\RFVRQ PILQYRWDMHRLGEPTGQGMKR RE*WKRIGEEVRQLMEKSWRGKSQ L\SH\SLRGESGTDPPSPMTHHD*VF ALMPLNP
1504	7001	A	1621	3	700	HASDRRHGSHACSRVSSGHQAGL LGGGWEEDRECGQRAEGMMFWA ALALAATSPSRLLLSPGKGPVPSRLL PLSDAASPTWLKLT*RR*RSQIYQT G\QEGPLLPSQIGVILRDSHGVA\QV RF\VTGNKIL\RLKS*GTCS*IFLIDL YHLN*ESQFAVRKGILRREQERDKG G*NFPSTDF*IGEAGFHPFWLRYKQ QAESSLPNWEIWNHLTASALGRINL VWCTPSN
1505	7002	A	1622	1	340	GEHSMAPPAHFRALLYHPGTATLV PHPASISQHSPSPWGNA/RG*PV*RQ RHLTAPRSPPHPRFRHKPGKDPREN PSRWPEVPSLPQTHVVPQGAAWDT VNTTVCKNRSTKPQD
1506	7003	A	1623	3	1076	HPVPSSYSVHTLSPAAMTEQMTLR GTLKGHNG\WVTQIATTPQFPENNL PASR\EKAILRKPARGWSQPMNFQ RRSRIHSHLLRMVVIS*DGQFC/AF QGFWDWKPCALGDLTNG/TPTRGR

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						FCGPIPKDVL.SVAFSSDNRQRLSLGS RE*THQSLWN\TLG\VCKFNLSRNE H/SESWVLCV\RLAPTTSKPLSIGLP VAWDK\LQV\WKPGNLCKADAPN PHLATTGFL\NTGDLSSSRWDPLCA SGG\KDGQA\MLWDL\NEGQPPLQR *NGGD\INA\LCFSPN\RY\WLCVAAT GPS\IKIWDLEGKI\VDDELKQEVISTS SKAEPPOCTSLAWSADGQTLFAGY TDNLVRVWQVTIGTR
1507	7004	A	1624	1	1189	LQGGGRRGCGASFSKPSAILVAAA THALAAAMTEQMTLRGTLKGHNG\ WVTQIATTPQFPENNLPAASR\EKAI LRKPARGWSQPMNFQRRSRRIHSHF V\SDVVIS*DGQFC/AFQGFWDWKP CALGDLTNGHPHEGDFVGPYPRNV LSVA\LSSDNRQRLSLGSRE*THQSL WNTPGWCANTTVPG*EPTQEWV\S CVPLPRPNNQQTPIHVLWPGNNLV QVMETWANCKLKDPT\NHWPTPGY SETPVTVLSRMDPFCA\SGGQGMAQ AHVYGD\NEG\KHLHARMVGTSI NA\LCFSP*PATWLCAATGPS\IKIW GFRGERSIVDELKQEVISTSSKAEP QCTSLAWSADGQTLFAGYTDNLVR VWQVTIGTRLEVYGRALPIKKKTGF SEKKKK
1508	7005	A	1625	3	445	GEFADSF/SSMGSPVNAQDFCTDLA VSSANFIPTVTAISTSPDLQWLQPA LVSSVAPSQTRAPHFPGVPAPSSGA YSRAGVVKTMTGGRAQSIGRRGKV EQETDQLEDEKSALQTEIANLLKEK EKLEFILAAHRPACKNPDDLGFPE
1509	7006	A	1626	7	514	
1510	7007	A	1627	3	462	RRSERAVTVLLPSSASQRPPVSAPRP LARLCLTATMMFSGFNADYEASSS RCSSA\SPAGNSLSYYHSPRRPPFSA WGSPVNAQDFCTGPGPFSSANFIP TGHLPSWTSPDLQWLQ\PALVSS V\APSQTRAPSTFSESPPPTAGA\YSR AGVVKTMTGGRAKSIG\RRGKVEQ LSPEEEKRRIRRERN\KMAAAKCR NR\RRRLTDTLQA\ETEQL*DERTAF WTRMSHPVEEEGKLEFILAAHR\PA \CKIPDDLGLPRKRMSVASLDTGG LPRGLPPRRSEEAFTL\PLLNDP*/DP KPSVEPVK\SISSMELKTEPFDDFLFP ASSRPSGSETARSVPDMDLSGSFYA ADWEPLHSGSLGMGAHGHGWEP LCTPVVTCTPSCNCLHVFLRLHLPR G*LLPQLCSCPPQGGQQQ*AFL*LA QLTHAAGPVRGQGRGGRHPQVPL PELVHYREEKHIFP*RVPRPGIASLT TTHPADLLFQHGARLSTRDFCTGP GPFSSANFHSGLAILDQSGPCSG WCKPALVSSVGPIADQSPFNLFQVP TPYRWGLAPGLAL
1511	7008	B	1628	43	674	MDWTWSILFLVAATTGVHSQVHLV

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						QSGAEVKKPGASVKVSKASFNSF DTYGFNWVRQAPGQGLEWMGWV SAFNGDTNYIRKLQGRVTMTTDSST STAYLELRSLKSDDSAIYYCAATNS DKYFWGQGTLVTVSAASPTSPKVF PLSLCSTQPDGNVVIACL VQGGFFPQ EPLSVTWSESGQGV TARNFPPSQDA FGDLYTTSSQLTLPATH*
1512	7009	A	1629	3	1639	SPGIFRGFQSVIRTEQRELTMESGLN WLLLVAVLKGVCQEVQILESGGGQ VQPGGSRTLSCAASGFIFSNYVMTW VRQAPGKGLEWVSSTAASGANTFY AESVKGRFTVSRESENMMYLQMS SLRDEDTGIYYCAKGDV PNLGVA WIVAGPGNVRPRK WFDAGWQGTT VTVSSASPTSPKV FPLSLCSTQPDGN VVIA\SCLVQGGFFPQEPLSVTWSESG QGVTARNFPPSQ\MASGDLYTTSSQ LTLPATQCLA\PKSVTCHVKHYTNP HPDVDG\PCVPSTPPTP/CSLNSTYP ISLMLPPPTVTAPTGPSKDLFLGSEA NLTCTLTGLE\NASGCHFQSEGLQV GKSAVQGP\PEA*PSVAAYSVVQLS CRGWREAMEPLVRPFTCTAA\HPV VQGPALTAHPLQNP GNTFPGRVHP FAPAVGRVCPFNDLLTLHCLAR\AF SPQGPCWVRWLQGS PKLP PRKST*L G/PFPAGA QARAPTTFAVTSILGR/V QPEDWEE/EGTPFSCMAGHEALAL AFTQKTIDRLARKPTHVNV\SAVMP EVDGTCY
1513	7010	A	1630	3	497	SSGPTRLRENHPWLLSPADKTTVKG PL/WGKVGAAHAAEYG\SEALGEGFS LSFPQPPKTYFPATSDLE/HNGFAPG LKGHGQRKFGRT*PKSRGGNVD\D MPQTALSAPERPCTAHKL RVDPV\ NFQASLSHC/LCLVTLAAHLPAEF/T PAVRLLWSKFLAS\VSTVL
1514	7011	A	1631	9	489	NSARATDSERTHHGARLLPDKTKA QRPPRLKLGANA\GEYG\SEAL\ERM FLSFPNPPKTYFRQFRP*ANGFAQG* RGHGQRRWPDALTQ\AVA\HVDEH APNGAVRP*SDLH\AHKL RVDPVN FQASLSHCLAW*PWPAHLPRPSSTP GGATPSLEQSSWASC
1515	7012	A	1632	2291	2960	INCPAQAKVADILQFNFKKFVCLF/D FLRQSLALSPRLQVQWYDLSSLQSP SPRFKQFSCRLRPSS*NYRCASPRPT NFLIF/M*RWGFTMLARLVFVLLTSS DPPTSA/SHSAGITSVSHCTRPLQSIFI *PLEQVS*VKDKNNNNKKT HFFVLFC FLRQSHSVTQAGMQWHDQSSLLL QPRLKQFSHFRLSSWYYRCLANF *IFCKDGVLLCCPW*SQTPGLK
1516	7013	A	1633	1	1233	
1517	7014	A	1634	233	884	ESPGVGCSARRGPRPRSPGPPPAAP GTPRPHGIPLYTRAGHQ**GEIRRRP CTFISKFLRPQGSASERQLPDLQAR

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						AWQELLGRPFNKHWHWFR*SPCKG IGVTRC\LRINP*KWIPLIGPGQHS LSSQELFRLLP\SEL\TLWG*PIEVS YRIGEDGSHLCACMKPSPA\GGSTQ NQT\NVQM\VD\SRISCKEELLGRTE PFPKTTNMMTVSG
1518	7015	A	1635	2	402	SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRLVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLTISKYR
1519	7016	A	1636	2	522	GLEFGTSHRLRENPPWCLSPADKTN VKA\AWGKVGGAHAGEYGAELER MFLSFP\TTKTYFPHFD\LSHG\SAQ G*RAHGK\KVA\DALTK\VA\HVDD MP/HNGAVPPLSDLHGAQAFGWDP VQLQSS*SHLPCW*PLARPPSPA EFQPLAVATSSLGQSFLGFLKKHRC LNLPNYR
1520	7017	A	1637	344	742	GFLIGVNEKTCFFTSPMLHDSYFFFL VNVIRCHFICGTYLYWAKHIFSVPF FLSFLFTSFISLFLPFPFFLFFFFFW *LLLPTPFYVSF\MKG*SFNF*FFI KCRLLTLLQNIK*TREMTTFDYFLSV FL
1521	7018	A	1638	1	519	PLKRS DGCNDGRPTRPPTRADTTAY TSNLKQTLVHLTTEEKSAVTALW GKVN\VEKVGKALGRLLVVYPWT QRF\FESFGDLSTPDVVMGNPKVKA HSQESSPRGL*WWAWLTWDNLKG TFAHTEVSLHCDK\LHRGSLKNFRL LGQRAW SVVAGPIHFVQKNFNPTS CRLA
1522	7019	A	1639	3	452	
1523	7020	A	1640	3	484	PTLLVPTDSERTHPWLLSPADKDQR QGPWVGKVGGAHAVRSMCAELER MFLSFPPTTKTYFPHFDLSHG\SAQV *GPRARKVADALD/TNAVAVGRTL PNALVRPL\SDLHAHKLRLVDPVQF SSFL\SHCLLG*PWAVHLRPSFNPW RLQGFLGDKVSWAFC
1524	7021	A	1641	180	613	SFAGISNGLAGRSVKDSGKAQ\AKA VSR\SQRAGLQSQWGR\INRH*KSRD AS\HERGGATA\AVYSA\ALE\YLPQ KVLELAGKASKDFKGKAYYPLRHL Q\LAIRG\DEE\DSLK\ATVAGGGVI PTTSHQISDRGGKKKDNTQKTV
1525	7022	A	1642	107	368	IYIILRD*VLSTFVCFILCKAIYKNIW TAFWKCS*ILICSI/LCNYVCTCTSVY ALCYIYIIDLRL*QQTYLCESKCTCIC MYVCIFLC
1526	7023	A	1643	790	1252	CAKPETQNNGNLRLRPLHFGHT LN*VRT*LKRRIFFFLRQSLALSPRV ECSGMISAHCKFCFLGSGHSPASAS* VAGTTARRQHAWLFLCVFSRDEFH RISKDGLNLL/NLVICPPRPPKVLGL QHEPPCPAKRRNFLSKIMGGHCFEL

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						SSCN
1527	7024	C	1645	171	329	MGARASGRSPLCQVGRQEQLRGR NGPLPASRLPQQPQVVPATPQSPRD DLA*
1528	7025	B	1646	196	514	MGRDTGPELCLHDSSLPAADDGPSL PTKQNEEFRPFIRRLPEFKFWHAAT KGILVAMVCTFFDAFNVPVFWPILV MYFIMLFCITMKRQIKHMIKYRYIPF THGKRX*
1529	7026	A	1647	43	321	
1530	7027	A	1648	35	821	GRPRLGRSGAASYRMSEGDVSGES VHGKPSVVYRFFTRLGQIYQSWLD KSTPYTAVRWVVTGLSFVYMIRV YLLQGWYIVTYALGIYHLNLFIAFL SPKVDPSLMEDSDDGPSLPTKQNEE FRPFIRRLPEFKFWDASVCGDGRCS CKAGGGRQCPVLAADAALTFSPHL K\HAATKGILVAMVCTFFDAFNVPV FWPILVMYFIMLFCITMKRQIKHMI KYRYIPFTHGKRRYRGKEDAGKAF GQLEAGLRLPHVLQEQQF
1531	7028	A	1649	156	818	HSYRMSEGDVSGESVHGKPSVVYR FFTRLGQIYQSWLDKSTPYTAVRW VVTGL\LSFVYIDSEFTCLQGWYIC* PMPLGIYHLNLFHKLSPKWDPSL M\EGLQDDGSFGYPTKQERREF/RA PFIRKGSFGVLNFWHAGYPRASLVA LWSCTF\FDAFQTSPVFW\PIL\VMYF HHASSCITDGRRANSRHMDSLRYR MPVSHMGK/RGRYRGKEDAGKAF AS
1532	7029	A	1650	154	685	PPLHLRDCFSPPGRALSPVGFYPYR\ RSVP\TWLKL\SDDVKEIQYKLGQ EGPLLLSQIG\VILRDSHG\VAQVRL G\TGHD\TFK\NLKSKGLAPDLPEDLY HLIK\KA\VAVRKH\LERNRKD*GC* NSRLILIESRISPFWLRYYK\TKR\VL PPNWEIWNHLTASAPGRINLVWCT QAIK
1533	7030	C	1651	127	435	MAASXNPEVLDITEETLHSRFLGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALS\VETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCCSP S*
1534	7031	A	1652	1	689	KCFI/VGADNVASKQMQQIRMSFRG KAVC*WGKNTMMRKPIRGHLENNP ALEKLLPHIRGNVGFVFTKEDLTEIR DMLLANKVPAAARAGAIAPCEVTV PAQNTGLGPEKTSFFQALGITTKISR GTIEILGVRNVASVCLQIGYPTVASV PHSIINGYKRVLALS\VETDYTFPLAE KVKAFLADPSAF/VAAAP/VAAATT AAPRAAAAPAKVEAKEESEESDED MGFGLFD
1535	7032	A	1653	68	1110	RTAVMPREDRATWKS\NYFLKIIQLL DDYPKCFIVG\ADNVGSKQMQQIRI VPWGEACVLMGQKTM\MGQAHPK

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						GTL*NNPSLWRKLLP\HIRG\NLGFC FTQGGPSLEIKGHVCLANKGLPSWL PVVGANCPHGEVTGGQPQNTG/LSG PEKTSFFPGL*AITTK\ISQGAPIENPE VNVPAESRTGDQSGKPSEANAA*TC SNISPF\SFGAGSSQPGVSTNGSHLPP LKGLDIHRRNLCIFWLSWRGVRNV AKCL SARLAYPTVA\SVPHSIINGY KRVLA\LSV\EPDYTFPLAEKVKAFL \ADPSAFVVA\VPV\VAPPAAPGG\ VAAPAKVEAKEESESEDEDMGFGL FD
1536	7033	A	1654	1	364	
1537	7034	A	1655	70	253	
1538	7035	A	1656	151	657	APTTPTGPGDPLDLVALAEQVQKA DEFIRANATNKLT VIA\DLQ\HLPE QARKVLEEHRDANLHHVACNIVK KPGDIYYLL* TGRVGGQYFISIIPKE LGDKFVHIDFLGAYKLQHDLSWTP V*GH*EGKMLKISMMGHVAKPVSG PASVHWNPTFQGTDSLEEWGF
1539	7036	A	1657	345	547	GFKPPDFFLCNENKWRKINTSSSE Y*CLMHIHLLIFNITIFSS/LHTYIHKH THTHTPFSVFIMEGC
1540	7037	A	1658	228	900	PSQAGNTSPSGARSSFPKDMKLLN SSFEAINSQLTVETGDAHIIGRIESYS CKMAGDDKHMFKQFCQEGQPHVL EALSPQTSGLSPSRLSKSQGGEEEG PLSDKCSRKTLFYLIATLNEFQA*L *LQHSPQPLSSAGSPALSWLG*MQS TAVCSQLCGEDFKDLKQPLWNAV RGDLPGLKCDIYS\YNPYLSDP/VG EDGSLWSFNFFYNKRLKRNRL
1541	7038	A	1659	35	1288	
1542	7039	A	1660	1	1641	
1543	7040	A	1661	212	369	HPVTVYLLLG YLLFQLPCGSEFSTSE THGHSADRLG\AAFAVSRLEQDEYA PG
1544	7041	A	1662	63	255	VLMFSSSHG*GYQSS\RLQCKLQIVQ LIQDILLFFSF* IPE*LLS*LTPLKIFPL HQNGPSDFVS
1545	7042	A	1663	169	391	
1546	7043	A	1664	85	1534	KSSHCIKMGPQIFHKTSELVLPATSC PSCPDQNEEDVSQTQYKECCG\GG WCSHSIFAVWHFI*RPDAT*FGLEQ RLTGLLASGPVSLREVV*LYSSLGT VISGK*KTSNVG*RGLALGSWAFSD KYSWFTMFTWACISGPTKAL\TTGV \GLIAF\GQCDVIVAGGVELMSDVPI RHSRKMIMLMLDLNKA KSMGQRLS LISKFRFNFLAPELLAVSEFSTSETM GHSADRLAAAFV SFLADQDEYALR SHSLSKKAQDEGLLSDVVPFKVP GK DTVTKDNGIRPSSLEQMAKLKPAFI KPYGTVTAANSS/LLTDGASAMLI MAEEKALAMGYKPKAYL/RRDFM YVSQDPKDQLLLGPTYATPKVLEK

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						AGL\TMNDIDAFEFHEAFSG\QILAN F\KPMDSDWFAE\NYMG*KKPRFGL PPLWRRFNNWG\GSLS\LGHPFGT GCR\LVMTAANRLRKKGGQYGLV AACAPG\GQGSATDYVEAYPK
1547	7044	A	1665	294	823	
1548	7045	A	1666	3	1171	
1549	7046	A	1667	1419	1801	TMEIHPIEQLDPSDHLESTAAGQEA LFTYHSF*STFISFFETGPHFVTRLK CSSAIITHYSVELLGSSHPPTSASWV AGNTGVCPhVQLIFLFFVEMGSHY VARLVFNS\GLVIFLPWLPKVLGLQ V
1550	7047	B	1668	68	471	MVRKLIVPRAEAAEAGGLPELGGH RPQPARAARAAALTGCSGGEDYTR YNQLSRAVPVCSRLGAHARVRWEL CDFVTASSFCRRRLPTVLLKLRMAQ HLQGSIAL*
1551	7048	A	1669	2	359	
1552	7049	A	1670	1	585	PRGVIGHGPLGTSFIGKYGCGDYW VKAFLDRPSQPN\QGPKKNFEVWD LVDVNT\DLMA\PVSAKKERKVSC MFIPDGRVSVSARIDRKGFCGDEIS IHADFENTCSRIVVPKAAIVARHTY LANGQTKVLTQKLSSVRGNHIISGT CASWRGKSLRVQKIRPSILGCNLR VEYSLLIYVSVPGSKQVFIKAL
1553	7050	B	1672	21	410	MPSKVRCXSVQVFDAMKTATAVA HCKRGNGLIKLEPVLGKERFAG VDTRVRVKGGGHVAQIYAIRQSISK ALVAYYQKYVDEASKKEIKDILIQY DRTLLVADPRRCESKKFGGPGARA RYQKSYR*
1554	7051	A	1673	1	456	MPS/KGPLQSVQVFGRRKKTATAVA H/CKRGNGLIKVNGRPLEM/IEPRTL QYKVLGSGTGVSGWRTLGD RDVV ALESWGAGISNGMFRSCVGCQWA AGASSASRQERFAGVDIRVRVKGG GPWPRFMSKKFGGPGARARYQKST DKPIVTQNSLV
1555	7052	A	1674	172	661	LLEPVLGKERFAGVDIRVRVKGG GHVAQIYGESQELGAWRRWLWEG GLHSAPVPFNCVSFSQLSVSPIS\KAL VAYYQK\WSEHGSFP*GRWVCGDQ VKDSV*LKSSSLFLPDVDEASKK EIKDILIQYDRTLLVADPRRCESKK FGGPGARARYQKSYR
1556	7053	A	1675	27	554	STLGAMPSK/GVPLQSVQVFG\RRK DSGQLLAH\CKRANGLIQG*TTGGPL EMIEARARLQYK\LEPVLGKVE RFAGVDIPCPV*KGGWSTWPQIYAI RQS\ISQKPLVAYYPEM*VSMGPSH E/YVDEAFQRREIKDILHPSY\DRNP AGLAGPFVRCE\SKKF\GGPGARAR YQKSYR
1557	7054	A	1676	192	836	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKL VFL\GLDNAGKTTLLHMLK

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						DDARLGQHVPTLHLTSEELTIAGM TFTTDFDLVGHE\QARRVWKN\YLPS QLMGFVFLVDCA\DHFSWSNPKVE LNALMTE*NNIPMCPILILGNK\IDR TDAISEEKLREIFGLYGTGPQERGEL *PLKEL\NARPM\EVFHVAVLLKEG KVYGRGFSAGLLPVLF
1558	7055	A	1677	196	520	DTVSRKNKSGKIFQLSSRV*YIERSQ SGVKVYKCKTFGKAFTQ/HF*AHM RMYTGEKPYKY*ECGKFFILVLLLL LMIQKYFHLLIKIVRLYLIRKKVSCKQ PSNKILQS
1559	7056	B	1678	1	1521	MGIRVTSVIVSRVPVPHSEAVFCCWL LGATDVWIPEHPANPRLTFPLFPESP GRHLREIKLQSARDASVKSANTR VIPKPQRVIHPGGQPTDKMDLDDL LNPRIIAAIKKAKLKSVEVLHFSGP DLKRLTNLSSPEVWHLLRTASLHLR GSSILTALQLHQKERFPTQHQRLS LGCPVLDALLRGGLPLDGITELAGR SSAGKTQLALQLCLA VQFPRQHGG LEAGAVYICTEDAFPHKRLQQLMA QQPRLRTDVPGELLQKLRFSGQIFIE HVADVDTLLECVNKKVPVLLSRGM ARLVVIDSVAAPFRCEFDQSASAPR ARHLQSLGAMLRELSSAFQSPVLCI NQVTEAMEEQGA AHGPLGFWDER VSPALGITWANQLLVRLADRLREE EAALGCPARTLRVLSAPHLPPSSCS YTISAEGSWG TNCKQNTRLHISPET AGPAAHAACWPQQD TVRAGHSES WHASCCNPDTDMQGGQTISTSVNQQ QEAQAKPPPTPL*
1560	7057	A	1679	991	1367	AVLVFNNGEANEGSGRGP*GERS SRARPP/SGPGPWNCAPRPWCPL RGWSSVSWD*TAQAKPVCKSP/AG GSSPGTGSPSAPSPGAGTEPAWAG PAELPGVFSLNVLPLSLCLIF*SLAC LA
1561	7058	A	1680	313	429	CIESMVHGGENIFFAGHGGSHL*SQ HFGRPRQVDHLRSG
1562	7059	A	1681	552	792	GSASDYQSGIRTVGPRDWLCRRRA LDLDAARTQSVRAAEGKCAFLQMQ GPRVYTGPRPRRADHLRSGV*DQ PGQHGETP
1563	7060	A	1682	508	1085	CQHFGRPRRADHLRS\GVRAQPGQ HGETPSLLKILKLA/GHGGAPL*SQL LGRLRQENHLNPGGRGCGEPRSHH CTPAWETERDSISKKKTKTQVVICI* SLNLVREIKNKIGLTAE*ILQKNSL EDVSIIEI*NEGQRDGGKMDRAFLRS MQQYQAVQYMCNQSPRRVGD RM GRINSQKKCKTYTMNTIKHC
1564	7061	C	1683	46	516	MLSDPPARIRTRKGPTETVSRIPRP SPNGQGPVDSSPSGXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXX*
1565	7062	A	1684	2	100	
1566	7063	A	1685	2	814	PGYKKGPQETGSRIPRPNPSPNPLRVL WTAHLVAMAPGSRSTSL\LLAFALLC LALGFKEAGCPSQTVPLSRLF\DHG MVQGPSRVTS\CAID\TYQQFEETYIP KDQKYSFLHDSQTSFCFS\DSIPTPS NMEGSATRNPILELLR\SLLLIE\SW LEPV\RLRSIVPPTTWVYEH\GTAI DYHLL\KDLEGGHPTV*WGRLEDG KPPDLGKILKQTYSKFDTNSHNHDA LLK\NYGLLYCFRKDM\DKVE\TFLR MVQCR\SVEGSCWLLGCPSSIL
1567	7064	A	1686	3	452	
1568	7065	A	1687	3	516	PTLLVPTDSERTHHGACLLPDKTNV \KAAWG\KVGAGHAGEYGAELER MFLSFPT\TKTYFP\HFDL\SHGFCPGL RATGKKVADALTKRRG\HTWDDM PKRRCPP*SDLHAHKL\RV\DPVQLS SS*SHLPCWVTPGPAHLPRPSSTPGG CKASLGQSFLGFL\KHLRCLNLPNNV
1569	7066	A	1688	3	409	SNFRSNFGYNIP\KHLADRVAMYV HAYTL\YSAVRPFGC\SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIYIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
1570	7067	A	1689	2	437	
1571	7068	A	1690	126	409	ILLWMDILICTDFGSVNYFNVWRL PKSYLSLFYSRIYIVHDEVKDKAFEL ELSWVG\ELTNGRHEIVPKDIREEA KYAKESLKEEDESDDDNM
1572	7069	A	1691	516	564	
1573	7070	A	1692	224	344	ILLGFLVLASDHLQSKYAL*CPLR HLP\ELNPSLREGSVL
1574	7071	A	1693	1	1237	MGCRPVGGAGLELLTSARTCFVSD LKRGLKIQAAKFNIDGNNECPIDTR KQLAENLVVIGGTSMLPGFLHRLLA EIRYLVEKPKYKKALG\TKTFRIHTPP AKANCVAWLGARSLLGYNRFLMF QPFRGEETVWSLLPKIQA\YCCPFL KYDLSASTFSPDGRVFQVEYAMKA VENSSTAIGIRCKDG\VLGV\EK*VL SKLYERRVPNKKTF\LMFDR\HVG M\A\VG\LLADA\RLADIAREEASNF RSNFG\YTIPLKHLADRV\AHVWCHA \YTTLPVAVRPF\GCQFPC*GPYSVN DGA\QLYHD*PHPGVSIPVNWGCAI GQRPGQAWQRRKLEK\QMKEMT\ CARDIVKEVAKIYIVHDEVKDKAFE LEPSW\VGELTK\GRHEIVPKDIREE AEKYAKESLKEEDESDDDNV
1575	7072	A	1694	1	1083	
1576	7073	A	1695	138	545	RPGMWSTRSPNSTAWPLSLEPDGP MASASTTMHTTTIAEPDPGV\GLP\ DGRMETPTPHP*LTMVVMAGCDV/

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						AAVPIVLVSLLFVMLRYMYRHKGT YHT\NEAKGTEFAESADAALQGDP AL\QDAGDSSRK\EYFI
1577	7074	A	1696	2	498	
1578	7075	A	1697	41	510	APSPRRPWGHFTEEDQGLLSTSLWG KGEMWKKCWEGRNPWERLPGCPT PWTPRGSFELWQPCPSA/ILAHWP ANPQSPRRHHGK\KVLTSLGRCP*STL DDLKGTFAQL\SELHCDKLHVDPEN FKLLG\NVLVTV\LAHF\GKDFTPGG CRASWAEDG
1579	7076	A	1701	153	744	AVNLVPSKDRHLTQSRSSQGGGVAN PNSGVYSARPSSPPQIALPAWGTG QPQTLQTSPGEGFSVQTGAEVGVG RG*PRRRPPRARQGGKGVHSTLKKL KHYRFHIADGLDRGQAPPLGRPLFL GPGWLRTH*GRAGK/QNPQTVGDH PGAGAPPSSPALAVSL*/H/CTGLC*I PSPACSPGSPSPRRGSHSPDAWV DP
1580	7077	A	1702	35	569	
1581	7078	A	1703	509	2455	LPAATVLFTSSPNFQIQPNRTNGD VTKKIHDSLESSKISTLKGNLERGYF QPSWMTLRGVRLQLEVPADIVEIA RELELEVEPEDVTEFLQSHDQTLAD QKLLLMAEQRKWFLEMETTPGGD AMNIVEITINNLEYNINFVDKGAAG FERIDSNFERSSTA EWVTVKQTQAH PSGGIQEGIVIIRDGSRPYTTPEHLPV RPNVEEEDSDIDESSPFLRNYYKA AHSFIGRIRFKHSTSLREAFYIITSK EFFSAIRKLASSPEKGGGIIFTAINP FTRSINEIYKIQRRRGKERQLNDCV HRSDDANKGPESLGSAGSGQSHDV AQGHLQGLVLGQLFILAPLGKFHPE EDVKQATSNFENLQQLARKMKLP IFIADAFTARA FRGNPAAVCLLENE LDEDMHQKIAREMNLSETAFIRKLH PTDNFAQKNMNSTLTFVTLSGELRA RRAEDGIVLDLPLYPAPHPQDFHEVE DLIKTAIGNTLVQDICYSPDTQKLLV RLSDVYNRSFLGEPGKLNTEENLLQV ENTGKVKGLILTLKGEPGGQTQAFD FYSRYFAPWVGVAEDPVTGSAHAV LSSYWSQHLGKKEMHAFQ/SFPPSE ESWEFPFVQT*RVDIRGCAPVVLEG TLTAYRWLCCDA AVSNHQVFSA
1582	7079	A	1704	1	1503	
1583	7080	A	1705	1	635	
1584	7081	A	1706	1	804	LQFSSALGGGRCRASASSPRRARRR GQRPRHPAPRRPQAARPSAAPRARR FLSQRPA AAAAAA QRAALMQAICV VVVGKPKL*GKT\CLLASYTQTCHF LGEYIPTVFDNYSANVMVDGKTG EIWGLWDTAVQEDYDRVTPPYYP A/QADVFLFCFPFVSPASFENVRAK WYLNVRHHCPN\TPN\LVGTKLDLR DDKDTIEKLKEKKLTPITYPQGLA\

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						MAKEIGAVKYL\EC SALTQRGLKTV FDEAIRAVLCPPPVKKRKRKCLLL
1585	7082	A	1707	1	848	RPRVRAGAENMMFSAARLSPWE GSPSFAENMNDWMPIAK\EYDPLKA GSIDGTDEDPHDRAVWRA\MLARY VPNKGVI GDPLALTLFVARLNLQ\TK EG\K*KEV\FPRYGDIRRLRLVRDLV TGFSKG\YAFIEYKEERAVIKAYRD ADGLVIDQ\HEIFVDYELERTLKGW IPRRL\GGGL\GGKKESG\QLEFGGR DR\PFRRKPINLPVVKNDLYREGNRE\ RRERSRSRERHWD\SRTRDRDHDRG REKRWQEREPIRVWPDND\WRRER DFRDDRIGREKKERK
1586	7083	A	1708	3	3067	
1587	7084	A	1709	148	4435	GIQRKYLKGSIMVSSGCRMRLWFI IVISFLPNTGFSRAALPFGLVRRELS CEGYSIDLRCPGSDVIMIESANYGRT DDKICDADPFQMENTDCYLPDAFKI MTQRCNNRTQCIVVTGSDVFPDPCP GTYKYLEVQYECVPYIFVCPGTLKA IVDSPCIYEAEQKAGAWCKDPLQA ADKIYFMPWTPYRTDTLIEYASLED FQNSRQTTTYKLPNRVDGTGFVVY DGAVFFNKERTRNIVKFDLRTRIKS GEAIINYANYHDTSPYRWGGKTDID LAVDENGLWVIYATEQNNGMIVIS QLNPYTLRFEATWETVYDKRAASN AFMICGVLYVVRSVYQDNESETGK NSIDIYINTRLNRGEYVDVFPNQY QYIAAVDYNPRDNQLYVWNNNFIL RYSLEFGPPDPAQVPTTAVTITSSAE LFKTHSTTSTTSQKGPMSSTTVAGSQ EGSKGTKPPPAVSTTKIPPITNIFLP ERFCEALDSKGIKWPQTQRGMMVE RPCPKGTRGTASYLCMISTGTWNP GPDLSNCTSHWVNQLAQKIRSGEN AASLANELAKHTKGPVFAGDVSSS VRLMEQLVDILDAQLQELKPSEKDS AGRSYNKAIVDTVDNLLRPEALES WKHMNSSEQAHTATMLLDITLEEG AFVLADNLLPTRVSMPTENIVLEV AVLSTEGQIQDFKFLGKAGAGSSIQ LSANTVKQNSRNLAKLVFIYRSL GQFLSTENATIKLGADFIGRNSTIAV NSHVISVSINKESSRVYLTDVPVFTL PHIDPDNYFNANCSFWNYSERTMM GYWSTQGCKLVDTNKTRTTCACSH LTNFAILMAHREIAYKDGVHELLLT VITWVGIVISLVCLAICFTFCFFRGL QSDRNTIHKNL CINLFIAEFIFLIGID KTKYAIACPIFAGLLHFFFLAAFAW MCLEGVQLYMLVEVFESEYSRKK YYYVAGYLFPATVVGVSAAIDYKS YGTEKACWLHVDNYFVSWFIGPVTF IILLNIIFLVITLCKMVKHSNTLKPDS SRLENIKSWVLGAFALLCLLGLTW SFG\LLFINE\ETIVDGHISFT\IFNCFP

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						GGVFHFPSFHCALPKGKVRKRIMA KCL/RRHLHTACGGP/LPT*ESPHSS VKASTHPEPSARYS\SGTQSRIRRM WNDTVRKQSESSFISGDINSTSTLNQ GHSLNNA\RDTSAMDTLPLNGNFN NSYSLHKGDYNDVQV\DCGLSLN DTAFEL\MIISELVHNNLRGSSKTHN LELTLPVKPVIGGSSSEDDAIVADAS SL\MHSDNPG/VWELHHK\LEAPL\I PQRTSHLLYQPQKKVKSEGTDSYVS QLTAAEDHLQSPNRDSLYTSMPNL R\DSPYPESSPDMEEDLSPSRSENE DIYYKSMPNLGAGHQLQMCYQISR GNSDGYIIPINKEGCIPEGDVREGQM QLVTSL
1588	7085	B	1710	98	264	XQVVCKKYRGFTIPEAFRGVHRYLS NAYAREEFASCTPDDEEIELAYEQV AKALK*
1589	7086	A	1711	155	1217	DPPSPVPAPPSSPRDGHFLVPDATM AEEQPQV\ELFVKAGSDGAKIGNCP FSQRLFMVLWLKGVTFNVTTVDTK RRTETVQKLCPPGGQLPFLLYGTEVH P\DTTKIEEFLEAVL\CPPR\YPK\LAA LNPEVQHSWGWDIFAKFFLPNIQEF QTPALN*QSGRRGFLESP*KVLDNY LT\SPSPPEEVDETSC*KIEGVSQARK FLDGQRRPHPWLDLQTCCPKVTH* VQVV\CKRK*PGNSPHPPKAFPGKC HRVP*SKMPYAPGKNSPSHPVPDDE EIELRPMKSKAKALQISPSLGLPSTP SIFSTKAPGGFHATPMGHTPKLASG QGILGDIETPAKGVVEEGMRERNGGP GSDF
1590	7087	A	1712	39	256	LSVKMEEGILPCSLYETTITDSKT*Q G*YI/EDFRLVFLINLNAIYLLKMLV NHLR*NMRDNSETYRIRIV
1591	7088	A	1713	1193	1436	PQSDFLDTLPQTSPHPI/*EVPTGLVC YSSRVNKRAPPASIPVACSPSPV SNPPHPVSNPPHVSAPLPCSSHQTQ QAP
1592	7089	A	1715	2	533	ARDSFLAAMASHR\LLLLCLAGL\VF VSEAGPTGTG\ESKCPLMVKV\LD\A VRGSPAQMWP*HVFRKPR**PPW EAILPSGTRKTQLSLGEL\HGAHKL EGICTNGIYKSGK*DTKFFTGGKTL GIFPHFPLRHCQEVGISTGQRTSGPR RLTPLAALLEPLTPISTTGCSFTNSQ GN
1593	7090	A	1716	38	661	APSPRRPWVISQRRTKATITSLWGK\ VNVE\ DAGGETLGRILVVPMDP RGFFDSFGNLSSASAIMGNP\KVKA HG\KKVLT\SLGDAIK\HL\DDLKG/T PFAQA*SELHC*QACNVGS*GTFKL PGEILLVT/LFWAIPFSGKEFHPLRCQ VFLGQEQKMAEDGD\WSGQCPCSF QITTEL TGP*MQSFSRIWLYSCKQLQ IINLFLLRDHQ
1594	7091	A	1717	32	487	SRRHGSSLWGKVNVEDAGGETLGR

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						LLVVYPWTQRFFDSFGNLSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1595	7092	A	1718	41	597	APSPRRPWVISQRRTKATITSLWGK \VNVE\DAGGET\LGRL\LVVYP\WT QRFFD\SFGNLSASAIHQPPKVQ GTWSKKVLTFLGEMP*KHL\DDLK GHLLPKPEVNLHC\DKPAMWDPIEN FKAPGEMLLVTRFWAIPFSAKEFHP WRLAGLPGQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG
1596	7093	A	1719	3	573	HSLFGTSEVINKLLVPDAHGSFHRG GPRLLSTSLWGKGECGKMEEKPL GRLLVVYPWT\QRFF\ESFGNLVLLP SCPSMGQPPKVKAHGKRRRC*LSLG RCQ*STLDDL\KGTFPCSLKRNLC* QACNVGS*RTSKLLGENVAG*PVFG QFHFRANKFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH
1597	7094	A	1720	676	1283	QRKILYTHNTTENKWEGINFT*SFR IFLFFLRRSFTLVAQAGVQ\WLDLGS LQPLPPRFKQFSLGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFSLTVSGVQWRDLGSLQ PLPSGFKGFSLSLPSSWDYGCPPPS PANFCIFSRHGFSPCWSGWSQTPDL K
1598	7095	A	1721	41	669	APSSRRPWVISQRRTKATITSLWGK \VNVE\DAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSASA/LSMGKPPKS KAHGK\KVLT\SLGDA\TKHL\DDLK G\TFAQA*SATCTVDKLHV\DPGGT FKLLGENVAG*PVFGQFHFRANKFT PGGCRASWQKQKMAEDGDWS\GQ CP\VLQIPLKLNC*MQSFSRIRLLFL QAITNNKSISAKRSP
1599	7096	A	1722	2	307	TPYLVGQVVAGAQAQLQFESHAGH LGPQLFNKFALPYIRDVAKQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM
1600	7097	A	1723	20	473	AVEFEANGLGPQGFPKNDIFL*A AWGEETDYPVWCMRQAGRYLPE FRETRAQAQDFFSTCRSPEACCELTL QPLRRFPLDAAIHFSILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGQVVA GAQAL
1601	7098	A	1724	3	1170	CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPKNDITFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFFSTCRSPEACCELTLQALGME VTMVPKGPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG

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						RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPQASHQLLRIL TDALVPYLVGQVVAGAALQLFES HAGHLGPQLFNKFALPYIRDVAKQ VKARL\REAGLAPV\PSIIFAKDGHF ALEELAQAGY\EVVGLD\WTVAPKK AREC\LGKTVTLQGNLDPALYASE EEIGQLVKQNLDTFGPHRYIANLG HGLYPDMDPEHVGAFFVDAGHKHS RLV*QNMWGWLWMLGINTHVWFD KTECIPLPSRTPNPDDWLFSGP
1602	7099	B	1725	92	846	IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHGLYPDMDPQHVGAFVD AVHKHLRLV*
1603	7100	A	1726	1	804	
1604	7101	A	1727	178	1093	TFLLPACLLAALLPLRHHVRGRAW VQGSILNEGVG*ALKDLINE\ACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NL S\MSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSDYEMK LMDLDVEQLGIPEQE\YSCVVKMPS GEYA\RICRESQPILGDAVVISCA\K DGSENFASGELGNET\IKLSQTSNV DKEEEA\VPIKMNEP\VQPNFCH*GY LNFFTK\ATPLSSTVDTPVCSADGTP LVGRSIIAGYGDHLKYLLGLPKDP RIEEGSLGHS
1605	7102	A	1728	58	483	AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQECQLYPRRSQQQV VVDFAELRQAFLAETPRGTVA AIAATASIAGAPTQYPPGRGTPPP RRQTTPPPGIM\APPPGMRPPIG/PPPI GFPLARGTPISMPPSGN
1606	7103	A	1729	292	531	FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLFPHFALIIANNKCIEQ KKKKK
1607	7104	B	1730	326	419	XRLTCKRSLARSIASLNAPQTDASGI SGGPDA*
1608	7105	A	1731	774	1763	GNPRSYLLSIAFPLGLQKAFKVFNC GTLDFGWNSNHDLFGKS\SKLLQ\HI DYRMRCILQDGRNFIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPR VEE/ESRVLGLVLLRG\ENLVSM TVEG\PPPKDT\GIARVPLAGAAEGPGV GRAAGRGVPAG\VPISPGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVA\ATASI\AGAPNTVPTQGT GTPAPTSPGRATQPPGIMAPPP\GM RPPMGP\PMGLRPARGTPI\GMPAPG \MRPPPPG\IRGPPPP\GMRPHKTL SILFDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC
1609	7106	A	1732	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM

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						GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1610	7107	A	1733	1	591	NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGK\VNVE\DAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAMWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQ\SFQ G
1611	7108	A	1734	1	477	RRPSWLVA AVLNRNANMQIFVKTLT GQNHHPRLRYETQ*HPLKNVQPKKIS KNKGGYPHPD\QQRLDNLPKGQLE GWPALLSDYKHPRKESHAPWCLR LR\GGHIEPFPPLPQKYLLRQR*SC RQVLCFAFNPPCLSTGRKKKCGSH QTTLRPQEGFRK
1612	7109	C	1735	9	254	MEFHSCCPGWSAMARSQTLAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV*
1613	7110	A	1736	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIIKILRHDIGATVHEL RDKKKDTVPWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG
1614	7111	A	1737	68	312	
1615	7112	A	1738	317	916	TSSPPSSLCFLSFSDICHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGELQYCLSEKPKLLPLELEK TGIQNYTVTEFQPLYYYVAESINDAK EKVGNSAATIPRPFVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE
1616	7113	A	1739	389	1881	NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQ\E TSY\EDNCNQKWVPISLDPPHLKER KLGALGPKYCALF\EENDVNLT\HIE SRPSRLK\KDEYGFPPFGIKRSLP\A LTNIIKILRHDIGATVHELSDKKKD TVPWFPRTIQ\ELDRFANQILSYGSG NWD\ADHPGFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEKKTW GTVFKTLKSLYKTHACYEYNHIFPL LEKYCASHEDNIPQL\EDVSQFL\QT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEKP KLLPL/ESLEKTAIQNYTVTEFQPLY YLAE\SFNDAQGEI*GTFAATIPRPF SVRHDPHTPQRIGGSWDNTQQL\KI LA\DSI*Q*IGIPFAVALQNIK

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1617	7114	A	1740	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
1618	7115	A	1741	1	360	SGACPAFLVDRNLRHHETTFNLMK CDVDIRKDLANTVLSGG\TTMYPG IADRMQKEITAL/APPSTLRFRFIAPP/ ERRKYSVWIGG\SILASLSTFQQMC LGKQEYDESGPSIVQRKCF
1619	7116	A	1742	13	1277	INPPPLSRRCQLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPISVGRPRHQGV MV GHGPRTDSYVGDEA/QRSKRGILT KYPIEHGIVTNWDDMEKIWHHTFY NELRV\APEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSG\DGVT TV\PILRGATTLLHA\NLRGPGGLARD LTDYLMKILT\ERGSFTTHGPSGKT FRNIKGEACATSPLDFEQEMGT\AA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIM KCDVDIRKDLANTVLSGGTTMDP G\IADKIAEGRSTALAAPAP*KIR\IA PP\ERK\YSVWIGGSILASLSTFPARF W\SKQE\YDESGPSI\VRKCF
1620	7117	A	1745	644	844	ELSPTTFMPFSEGAEHLYLPPGQPG* GSESPGGCPA/PPYPSYSAPPATPEP IEKSQPNPIRHRFP
1621	7118	A	1746	2	271	
1622	7119	A	1747	83	420	DSSNPSCQSPTQLSKANTLGWHVV CELALPDPQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGKLGPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGLSPDGPLP
1623	7120	A	1748	154	1030	SDISQAQLSCTGPPAIPGIPGIPGTPG PDGQPG\TPGIKGEKGLPG\LAGDHG EF\GEKGDGPVG\N\PGKKFGPKGP MGPKGGPGAPGTPG\KGDSDYK ATQKIAFSATRTINVP/LLRSQTIRF RPRCITNMNTN\YE\PRSGKFTLQGC PGLY*FNLSTPVSRGNLCVNLMRG RERAQK\VTFCGLMAY\NTFQ\VT GGHGSSAEE/GPQKEGGGGKRPFF LQATDKN\SLTGAWEGANSIFSGFL AFFQIWEGLTCGLASHPTAPPARN AHYTPNNNHMTKPNNAHNRDW
1624	7121	A	1749	3	607	FCPRGQEFGEKNKLLSPRRPWVISQ RRTKAT\NTSLWGK\VKCGKNAGKE ETPGKGSLLV\HPWTPRGSFEQLW QTCPSALCPSMGNPQSQGTMAKKV LTSLGRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVGS*RTFKLPGEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQ\S FQG
1625	7122	A	1750	2	585	AAAAPAGGNPEQRLDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPRAGSPASPAGCGGGKGGG

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						LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEPAAAPG PSIR/PVLPPIQTGS\WRRPKSLRPVL GTRVGRTPPLPPP/PDPAGPPPLPLPG P\HPSRPPPTGPWRPARADGRV
1626	7123	A	1751	25	1295	KLCATKDLSYLA AAA SPTAFAYLG GLFSPKLPVTMAHRFPALTP\EQKK ELSEIAQSIVANGKGIL\AADESVGT MGNRLQRIKV\ENTVEENRRQFR\EIL FLLWDSSIQPGGIGGC*FLFPRR/YPL TQKGTARGKLFPGNIPSREKGD SW VGNQV*DQGR LFLFCREP NKG NHH FKGLDGLF\ERFVQYKKG DGVDFGK WRAVLRIADS\CPSS LAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLAAVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVG YGSP*QALHRTGPAAV PG\ICFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYG\RGLQAQCTG LPWGGKAANKGGNPR TAFMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRLHLKPCLYPT
1627	7124	A	1752	1	186	IFSRDGA\HRVTQDGLDLLTS*SARL SLPKCSDYSREPPRAQTPILIRHFIH NSKHEKTME
1628	7125	A	1754	74	595	RGGQGLLSTSLWGK\VNVE\ DAGGE TPGKGS L VVYPMGPQRFFDSFG\NL SSASAIHGQTPKVK\AHGKKGADFP WDDAIKHL\DDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFP GQKDG* LGVGQCPCS FQ\PLKPLGP*IQ\SFQ G
1629	7126	A	1755	21	457	NPRVRGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSL LDAQ ADEAVL\DNKNSLEILLGSIGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTL SVQNTDSPSYPEISSSCSMEQL QDLGGKLDASKSLGKSTQL
1630	7127	A	1756	1	455	
1631	7128	A	1757	3	468	
1632	7129	A	1758	50	895	THASDGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSL LDAQ AD\EA VLDHP\DLKHIDP\VLKHC\ HAAA\ATYILEAGKHRA\DKSTL\ST YL\EDCKILTEKRIELFFAREYQ\NNK \NSLE\LLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRM\YRPA\YLG DLKV VQNTGIPPS\YPREL VFSCQPW NQL\QDL\VGETLKDASKKPWK RAT SVVTLGKVNRSPPSSRRKTQKPPLP FSWNHRLC RAGCPFSVEKNFSLNL YPFIHFGHFKNV
1633	7130	A	1759	470	737	RKSFFLAQTVLKWCCEKMSSPGKK LFPGEIWGVKGNKNKLWPLPDPSIR HRFERVPSHKRPLPGWVRWLTPIPS TLGGQSAVDHLRSGVRDQPGQHGE

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						TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGG\RGCEPRSHHCTPA WATE*NSWDYSCLPPRPANFYIFST DGVSPCWPGWSRTPDLK
1634	7131	A	1760	1	297	
1635	7132	A	1761	1	162	
1636	7133	A	1762	54	504	YTAIMSIMS YNGGAVMAMKGKNC VAIAADDRFGIQAQMVTTDFQKIFP MGDRLYIGLAGLATDVQTV AQRLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLNAV DRDAVSGMGVIVHIEKDKITRTL KARMD
1637	7134	A	1763	51	748	YTAIMSIMS YNGGAVMAMKGKNC VAIAADDRFGIQAARLLTTNFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGNLNLY*V*REG\RQIQTFITLM EAWLANLFVMRKRF\GPLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLRECV ESLWGGPTWVPDSTVLKTIFPRPWL NAVGPWQCSGMGSSLFHIEKDKI T\RTLKARMD
1638	7135	A	1764	433	851	KPQPFILCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN\ FFETESHVST*L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV
1639	7136	A	1765	213	617	KRFLV*KVASVLKGLHAI\VVSDRD GSTLLK WANDNAPEHAF/RGPGFL \STFALATDQGKQTWDFSKNKSNIC LLTPYQGGFNFN SFYLWVGEFS*A QAGSAQLQGLICSA*EKGTWFLF* RN*GQVVEVSLI
1640	7137	A	1766	2	140	
1641	7138	A	1767	157	371	
1642	7139	A	1768	3	135	
1643	7140	A	1769	1	1431	MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALVTASTDGIGFAI ARRLAQDGAHV VVSSRKQQNVDQ AVATLQGEGLSVTGT VCHVGKAED RERLVATAV KLHGGIDILVSNAAVN PFFGSIMDVTEEVWDKTLDINVKAP ALMTKAVVPEMEKRGGGSVIVSSI AAFSPSPGFSPYNVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCSEDASYITG ETVVNLSVMFTGGGVCRAASWKE GGTGTPTRPRESPRQREPGETSSTD QENKVWNGLPANPQRPA AEGPVRR KTNKQKGIASAKDSINIRTGKDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNWENKFDDLT DVSFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV

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						QELHEGYTSFNS
1644	7141	A	1770	53	582	RKETVSVSPQQSRHLIGVRS PKGLS EVALAGLIHAQGAATSVHCARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SA\ALAQIAGATSQGP/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARDLTL DIIG
1645	7142	A	1771	44	1059	AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHV VVSSRKQQNV D Q\AVATL\QGEGLSVTGTVCHVGKA EDRGAAWWPPAVKLHGGIDILVSN AAVNPFFGSIMDVTEEV\WDKTLDI\ NVKGPKP*MTKAVVPEMEKRGGGS \VVIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRV\NCLAPG\ LIKTSF\SRML\WMDKEKEESMKE\T LRIKKV*ASPEDCAG\IVSFLCSEDAS LHSLGKTVVVGGGTPVPASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPHSNQFLPL
1646	7143	C	1772	1	174	MWIFIFNKYYQHVKSPMSRTGKS ATCDGCGMAAHCRCWGLSWGLG EALSYSKNV*
1647	7144	A	1773	154	765	RAGLEELTAAVMVRLNCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMGKKTW\FSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGA\HFLFQKF*D\AMPLKLTEQPE LANKVDMVW\IVGGSSVYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD
1648	7145	A	1774	1	676	DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLLQDFSRN LSAKSSALFFGN\AFIVFAIPWLYW RIWHMDLFSKAVLYSVMT*LSTYL VAFAYKNVKFVLKHKVAQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\KNEV\ADYEATNIF PIFYNNTLF\VLV\IVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALLFTG SK
1649	7146	A	1775	99	362	
1650	7147	A	1776	3	403	
1651	7148	A	1777	184	360	
1652	7149	A	1778	1	885	EFGTRWDFSMVAFADLDRAGSDL KALRGLV\ETA AHLGYSVVAINHIV DFKEKKQEIEKPVA VSELF TTLPVQ GKSRPIKILTRLTIIVSDP SHCNGFER QLLRGARLYDVVAVF\PKGQEKSLF HIA\CTHLGCGDLV\CITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLLSR TPTMRKVYNFPSAPPILMPNLA KGK NVNYYLGGWQERAFREIR\GPYDV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GKS*ACLFPGPF*K*TPRVRVST\NCR A\LLHGETRKTAFGIISTVKKPRP\S EGDEDCLPASKKAKCEG
1653	7150	A	1779	175	534	DCSLPSVCHFPHPSPHTHPPTHPW /CPSSGPEGLPIT*RHQVGSCTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHMCNVVALTFYATYED LCCTCNKYIEKAHTSVW
1654	7151	A	1780	190	390	TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSC GV*CSWGQKSIRVSLLWGF
1655	7152	A	1781	805	1325	ASKLEGSPCGKGGVGLGGCFPKRPE PRNHPHFVLWYLPQTRLEPKPLP PQLPSVG*KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGFPACA TSSGKPKLKRPLCAKSTMP*THPPT VP\KPPGQEAVERNQAPMASEFPSSP SVSGDLKPWGFERSFLCQGGAWS
1656	7153	A	1782	1016	1560	KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYR FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGPSLFPHTPFL TTP/LPHG*LFPSAPPALHHATHFRT
1657	7154	C	1783	68	223	MSPSSVFFVXXXXXXXXXXXXXXX XRASFIPFLDLXXXXFFLSFQMKSI DF*
1658	7155	A	1784	1373	1651	LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLLISSNHI*I NVKAYIVLYVN*ILKITKYMILLSTT
1659	7156	A	1785	6	140	
1660	7157	A	1786	223	397	QTPP*KSKQPFRTSS*DQVPSQP*\PPI PPINNPPIPPPFGEVYYFEPILRKWV KGR
1661	7158	A	1787	2287	2854	
1662	7159	A	1788	1	610	SGRPFFFFLSGGARATAQLAESWRG GQHLQSSSPPPPPASPGGPSSDQRS PCSNARW/NTSIYSLVADGTC*D TALVGNKDP\PSIWAAPGKTFLNIT PAEVGVL\VGKDWVKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSP\TFNVIVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY
1663	7160	A	1789	157	610	GYRKKQLRGDRRWAIHRIRITLTSR NVKSLEK\VCA*L**RRRKKEKNLK S*KGP\VRMPTKT\LRITTKT\PCG*/ EGSKDRWDRFPD*GFHKRLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQISIHTIDDQLLKKKKKK KI
1664	7161	A	1790	1367	1582	METRWESPPPDNFIAPVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFRKCALQEKWFF
1665	7162	A	1791	122	344	ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFP

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						FRKSPSQVQAH*PGSDEDPRPL*EDPRPL
1666	7163	A	1792	656	1068	NQINFCLNGKYTYVCIDTLPLYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK
1667	7164	A	1793	138	396	
1668	7165	A	1794	143	327	CGVQLLPDRRRESRDIIIVEL*AAVA AAGGNPDGKKGGGGWEAGQRKER KESEDPDAEPDCV
1669	7166	A	1795	23	483	KAIVLLHIICTEVSIIILFNDFIQDKRP CRLFTCCSLLRSASPVSAAANMPPEL FSSTSSSTVSWSLSSSLSSCFLSFR FGNSSCMSFSIIIPFVRPEDWKRMLL AK*GPLMALMLCALFFSSSSRLKPL FMSTTILSLKYGGGVQDVGGWQ
1670	7167	A	1796	429	1394	TISFEADIHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFN\HW\ LKVPEAKLTDYLFVDRKLFGLMPS LLINDIEDNSKLPTWAFPVASIIYGI PSVINSANYVYFLGLEKVLTLDPD AAKLFTRQLELHHGQGLDIYWRD NYTCPT*EYKAMELQKTGGFLGLS KCLKHIVSDYQEYLKPLLNTLGLFF QIRDDYANLHSKEYSENKSFCEDLT EGKFSFPTIHAIWSRPESTQVQNILR QRTENIDIKKYCVHYLED\EGSFYET RNTLKE\EAKEYKQIDARGGEPLS LVA\LVKHLK*RCSEKWKNNV
1671	7168	A	1797	145	172	GGCLLESVDTSHGQSLLISASLNTK HPTGMHSTCWFHVELCGKGLGSRH TLKQHQSAF*SMPA/PPAPCHIVP/QE PTS*VHPCWVFCVETG
1672	7169	A	1798	197	378	VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET
1673	7170	A	1799	32	377	SSMPPTPGPSILSSLVPIPVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKSGGFCF
1674	7171	A	1800	168	224	
1675	7172	A	1801	224	527	CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRPDKYEYDNK*FIEIKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW
1676	7173	A	1802	22	430	SPGCRAESEKSQGSERGVPSPYRI WVGSGKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDYSVHCSGDGCTKVSEITTKN LFM*PKTTCTPKTTE
1677	7174	A	1803	386	511	
1678	7175	A	1804	362	439	
1679	7176	A	1805	776	1376	GAPWAFGGLPWVHGLAKEGVTAVI

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						AEHGLWNIGVHEGHGTLQLQMH HYAVALRRHPFIQAQAQRGVLAG GGMGTRRE*VRARGQPRVHSNNCH TGQNRYSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVFHFPGLSHIGEEHGL RGQLSTV
1680	7177	A	1806	420	508	
1681	7178	A	1807	735	841	
1682	7179	A	1808	796	1123	IQWICHNTISAPKNYLEISPHINNKK F*KKI*KHFPPA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS
1683	7180	A	1809	137	303	
1684	7181	A	1810	122	385	YPALEHILKAQAIQSRCGCDSCLPSS APWDHPGPTTP\SPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG
1685	7182	A	1811	77	1181	PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQTFLTADV*RSPKKSRSPRE SPKKAKKLEVIIGKPGSSSF*QRIR KRERTPATRA*SQKREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSDR KGDRDRDREREKENERGRRDRD YDKERGNEREKERERSRERSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRERSRERKHSRERSR NAGKRSRERSKEKSSKHKNESKEKS NKRSRSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND
1686	7183	A	1812	1	585	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEK\SAVTAL WGQA*TWMKVGGKALGK/RCWVV LPWDPKRSFEVLWGNLSQLP\DAVN GANP*R*KASMAKEKVLGCPLVNG PWL/HWTTLKGHPLPHTEVSLHCD K\LRGSLKNFRAPGATVGLCCLA HSLLAKEFNPNKLQGLPIQEKLVGW VVG
1687	7184	A	1813	505	671	QKNKVYFFFYETIEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPLC
1688	7185	B	1814	277	480	GTGHFYGRTPSDTNCQEYTHRKL CQIKSKADLVLMKNKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ*
1689	7186	A	1815	32	1386	VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSSRGVYSAYQAP DIHECCHFRSASFLLDKMATPAVPV SAPPATPTPVPAAPASAPASVPAPT PAPAAAPVPAAPASSSDPAAASAT TAAPGQTP\ASQAQAPATPAPALPG PALPGPFPGGRVV\RLHP\VLASIVD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						\SYERRNEGACPS*SGTLFGKLVDK\ HSVE\VTN\CFSVPHNESEDEV\AVD MEFAK\NMYETGIKKVSPNKLILG\ WYATGHDITEHSVL\IHEYYSREAP NPIHLTV\DTSLPGTGRMSIKA\YVST \LMGIPLGRT/LWGVMTPLTV\KY\ AAYDTERIRRLTLIMK\TCF*PPTRVI WTSQVDLQQEGGGIQLRNPGMPLS TSVANMPEGCTCLGKVSADNTIRK VGHFLMSL\VN\QVPENRKPMTFET MLNSNINDLF\MVTYLANLTQSR\IA LNEELVNL
1690	7187	A	1816	273	748	VIQNLFNKMDVGTGQVRVVHACNP RHFRRLRQEPKSGVQDQPDQHGET PSLLKIQKLARR/GGVVHL*SQLLRR LKQENRLNPGGGGCSEPRSHHCTPV *VTQ*DSVPPAPRKKKMYVVLTKK FHIWHISFTLPNIKRSDSLRNRKVT NFSCYCSKVS
1691	7188	A	1817	1	406	LCQLETYPPISQCTASDFPGPVTAS WAIQEAARSGQAKAGA/GSATLS/M AYAGARFVFSLV DAMNGKEGVVE CSFVKSQETECTYFSTPLLGGKKGIE KNLGIGKVSSFEK MISAIPELKAS IKKGEDFVKTLK
1692	7189	A	1818	1	1222	FRQRAGAGQCGRWVSHFRVTSSCA CYVDAPPAPAMLSALARA VPSACS/ LARSFSTSA\QNNAKVAVLGASGGI GQPLSLLLKNSPLVSRLTYDIAHTP \GSGPQDLS\HIETKSR*KA YLGTW NSLP\DC\KGL*WW*VIPAGVPTKP GMDRD\DLFTTNATIVGTLTAACAQ HCPEAMICV\ANPVNST/ISPITSKK VFKKAWGQHPQKSSGVTTLNIVR AKTFVAELKGLDPAGVNVPIITGGH AGKTIPLISQVHAYDPVRGFECTPK VDFP\QDQL\AALTG\RIQE\AGTEVV KAKAGA\GSATLSQCRNAGA\RFVF S\LV DANELEKERCLWECSLPLSPQE TECTYFS\TPLL\LGKKGIEKKKAKT\ LGIGKSL\PFEEK\MISAIPELKA\SI KKGEDFVKTLK
1693	7190	C	1819	876	1124	MALGLRQRGIVSLAASITGPCPMSP APSHPGTQVLLPTKRHPQVCLSHTC VEMRQVTKRLSAFKVRNKPDRFY SALLCSTE*
1694	7191	A	1821	103	483	
1695	7192	B	1822	1	798	MAFLDNPTILAHIRQSHVTSDDTG MCEMVLIDHDVDLEKIHPPSMPGDS GSEIQGSNGETQGYVYAQSVDITSS WDFGIRRRSNTESPKPEQLRNLFIG GLSFETTNEKRSHCEQWGTLPCDV VMKDSNTRSGGFGFVYATVEEV DAAMNARPHKRRKKYPLL GKNTN DKQLDLGPEKGRKHALNCHRMKP ALFSVLCEIKEKTGGATQAFAKENN QKAYKETYGVSHITRHDMLQIPKL AQNEKSQVPSIRSIQRLKII*

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1696	7193	A	1823	3	545	
1697	7194	A	1824	1	440	VYLHLHSSQDRLLPMTVVTMASAR VQDLIGLICWQYTSEGRKPKLNDN VSAYCLHIAEDDGEWTHDFTTLD NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVR\INAAHGFSLIQVD\TQKVT MKEILLKAVKRRKGSQKVSACD
1698	7195	A	1825	293	2142	GNWPTERMAFLDNPTILAHIRQSH VTSDDTGMCEMVLIDHDVDLEKIH PPSMPGDSGSEIQGSNGETQGYVYA QSVDITSSWDFGIRRRSNTAQRLE LRKERQNQIKCKNIQWK\ERNRSKQS AQELKSLF*KKNLSKEKPPISG\KQSI LSVRLEQCPLQLNPNFNEYSKFDGK GHVGTATATKK\TDVYLPLHSSQDR LPMTVATMASARVQDLIGLIC*QYT SEGREPCLKDNVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVR\INAAHGFSLI QVDNTKVTMKDILLKAVKRKKGFQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPIDSDLLCACDL AEEKSPS\HALF*LTYL\SNHDYKHS TFESDAATANIVLKVNYIL\ESRAS TAR\ADYFAQKQRKLEQTVRAFSFQ KEKEIPGSIEQLAFQPQILVPVASEP ACGPSALRSPPGVLSFGGEAHPL GPLGTGAGGLFGEGVGGPLRREA GDIAMGRKFALAMGF
1699	7196	A	1826	436	917	RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARDCNPNVRLKWEDHLSPG I*DQPGKQ*DL/PSLQKNKKLPRHGG \HTLWSQLLGRRLWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA\WIFCFVEMQVSLFS RLVSNWAQVILPLQPHSVGIAVTS HCTQPYVIL
1700	7197	A	1827	46	573	SQTPMGHFTEED\KATIT\SLWGK\V NVE\DAGGE\TPGKGSLVVYP\WTQ RFFD\SFGNLSSASAIHQTPKVKAH G\KKVLTFLGTMP\TKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNPIFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP
1701	7198	A	1828	1	388	
1702	7199	A	1829	75	520	TPERGSAYPRPLLCGAPPGEATVIM SDQEAKPSTEDLGDKKEGEYIKLV IGSGF\SEIHFKVKMTT\HLKKL*ES YCQRQG\VPMNSLRFLFEGQRIAD\ NHTSNKNWGM\EEEDVD*SFFREQT GGSFQQFRIFLFFFFSLKSFFIF
1703	7200	B	1830	78	236	MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT

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						DK*
1704	7201	A	1831	67	587	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIAGLQ IG\DKIMQVNGW\DMTMVTHDQA RKRL\TKR\SEEVV\RLLG*RGSRMQ K\AVQQSMLFLRQPPPSCLPLC TVTPLPHSGPHLASADRWAPASEGL
1705	7202	A	1832	3	420	HSLSGTSEVINKLLVQTPMGHFTTE DKATITSLWGK\VNVE\ DAGGETLG RLLVVYPWTQRF\FDSFGNLSSASAI \MGNPKVKAHGKKVLTFLGEMPLK HL\DDLQGAFAQA*SELALVDKPA MWDP*GTSKLLGEMLLG
1706	7203	A	1833	3092	3227	ERQ/WPGTVAHACNPSTLGG*GGG AGIT*GQEFKTSANTVNPSLL
1707	7204	A	1836	3	1088	SMAAVAAESACICRWRRCSTGQF EELLRLKAKSLLVVHFWAPWAPQ\ CAQMNEV\MAELAKELP\QVSFVKL EAEGVPEVSEKYEISSVPTFLAFKNS QK\IDRLGWVHMPQELTKKVQADM HLSGLLPTQALMEHL*RKILQPFGL EGNLTSLWAPLAWLFYWKELPSK EPR\CGFSK\QMVEILHKHNIQASSF DIFS\DEEVRQGLKAYSSWPTYPLA\ YSGELIGGLDIIKELEAEEELDTICP KAPKLEERLKVLA\TNKASVMLFMK GN\KQEA\CGFSKPNKGKYNSTW C*NLETFRIILEDERKFGQGLKSLTP NW\PNIPSLYVKGE\LVGGLDIVKE\ LKRKLGEFAAL*LRGEN
1708	7205	A	1837	3	703	VEFFSSQRAELYATPLTPAPGPNGGI PGWTLWLALPRPGNLRKGPGLSL QEVDEQPQHPLHVTYAGAAV/DDE LGKVLTPQVKNRPT\SISWDGLD/S KGKLYTLVLT\DPDAPKQKDP\KY RE\WHHFLGWSTLKGQMTSATGTV LS\DYVGLGGLPKGTGLHR\YVWL \YEQ\DRPLK\CDEPHPSATRS\GDHR GKIQRWASLPVKK**SSRAPGGWAP CYPQPEVGMNQCAPKL
1709	7206	A	1838	717	1390	ASTTSSVHCARTYMGSVYNTPAR VRLRVGWRAADQLLLAASSTSAI VSTRALECAKMQNAEADATLVFI GYVVPALATLYAAGATLPRSAGKD TPPGTGDHGPAGALGTQAAGGHRV HAVWALDATLSDPAGAHGHLAR EARGCTLPGGYCTL*RISPNSWSPA AL*HHFSTAT*TRASPASSNG**KSC PAG/APALLPGPHGGAAGAGVGGP ALLGET
1710	7207	A	1839	1	310	RTSPHSPRNILLLS/EPENADSLMLV DFEYSSYNYRGFDIGNHFCEWVYD YTHEEWPFYKARPTDYPTQEQLH FIRHYLAEAKKGETLSQEEQRKLEE DLLCM
1711	7208	A	1840	3	375	HYLAEAKKGETLSQEEQRKLEEDL LEMYSKDEMGNLRKLLSTPSPV

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						VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPPESET VQETGLFLSLSRSPWLAGQSPVLCM
1712	7209	A	1841	94	429	
1713	7210	B	1842	96	979	XVGEEPREVLLRLYGAILQGVDSLV LESVMFAILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLPKAPPPNP PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVLSSAAIATKMAQFHG MEMPFTEKPHWLFGTMER*
1714	7211	A	1843	5	1463	PEKPRPAGRGAERGRKEPSPSESG AHPGLGPGRARAMAAEATAVAGS GAVGRCLAKNGLQSKCPDTPKR RRASSLSRDAERRAYQWCREYLGG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSLVLLESVMFAILAERSLGPQ LYGVFPEGRLQY/IPTSWVQSRPLK TQELREPVLSSQAIATKMAQFHGM EMPFTKEPHWLFGTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDE\MGN LRKLLESTSPVVFCNDIQEGNILL LSEPNADSLMLVDFEYSSYNRYG FD\IGNHF\CEW\VYDLYSSE\WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPPRRSQKKNWKE\DLL VRKSSRVMFWQSHFLWG\LSWILQ\ ASMST\IEFGYLDLCPSLRFQ\FLLPS KKGQA*PSVHSCILDSTLPLLGFLE PPGQGPWRGGTTSRRPWRLG
1715	7212	A	1844	143	762	CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLPGMYPALMYQ MYKSRRGLKRSSEDSKETYPHRLI EKKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTLKHVKALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNFFFL
1716	7213	A	1845	203	1507	CRQERAVAPARRAMERIPSAQPPPA CLPKAPGLEHGDLPGMYPAHMYQ VYKSRRGIKRSSEDSKETYPHRLIE KK\RRDRTNECIAQLKDLLPEHLKL TTLGHLEKAVVVFELTFEH/V*KALT NLNLSSSRQKIAL\QSGLQAGELSG RNVETGQEMFCSGFQTCAREVLQY LA\KHENTRDLKVFASTHL\HRV VSELL\QGGTSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTDTDSGYGGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQESEEPPTKKNRMQLWDD\EGP FQLASDLNQLPPFPGPQPQHQPFFCL PFYLIPPSS\ATAYLPMLEKC\WYPTS VPVLYPGLNASAAALSSFMNPDKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD
1717	7214	A	1846	628	1061	AHRKSLYLCEACFPRSRASQETSGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPPKNSREQGFNDPVGQSV EPLEQPLFPWEWQWPALAQDREL
1718	7215	A	1848	88	953	FQAPQLCYDSAFMISSVPSPHILRVC EFPCFHAHLRVCEFPFHAHLVCVE FPCFHAHLRVCEFPFHAHLVCVE PCFHAHLRVASVNFHFHAHLVCVE FPCFHAHLRVCEFPFHAHLVPSVN FCFHIHLVCVEFSCFHAHLRVCEFP FHAHLRVSANFRVFTPTCASVNFV FTPTCVCEFPFHAHLRVASVCEFP CFHAHLQVVEFPFHAHLRVCEFP FHAHLRVCEFPFHAHLVCVEFP HAHLVCVEFPFHAHLVCVEFP AHLRVASVNFHFHAHLVCVEFP HAHLRVCEFPFHAHLVPSVNF IHLVCVEFSCFHAHLRVCEFP HLCVSA/CPCFHTHLCVCEFP HLCL*ISVFSRPPASVCECL/CN/CPC FHAHLQ/CL*ISVFSCPPAGL*ISVFS CPPACL*ISVFSCPPVCL*ISVFSCPP ACVCEFLCFHAHLVCDFPCFHAH QSATVLV
1719	7216	A	1849	1	254	
1720	7217	A	1850	3	308	
1721	7218	A	1851	1	380	IPTPLIGNFGPRGPRIRHERPQKRDD RREPSSFGKRRQ*DGTLCL\RRCGS\ KA\YHLQKSTCGKCGYPKRKRKY NWSAKAKRRNTTGTGRMRHLKIV\ YRRFRAWDFREGTTPKPK*GSLLQH SSSS
1722	7219	A	1852	41	544	APSPRRPWGHFTEED\KATITSLWG K\VNVE\DAGGE\TPGKGSVVYP\W TQRFDSFGNLSSAF\AHHGQTPKV KAHGK\KVL\SLGDAIK\HLDLKG TFAQA*VNLHL*QSCNVDP\ENFQA PGEMLLVTR/VLAIHF\GK\EFTPGGC KASWAEDG*LAVGQWPCSSRYH
1723	7220	A	1853	145	705	SWRNRTVSNBSAVSASSVHLCFAE CKALCGERILTDGSDVSRPTIAAGG CNGTVKYLL*QEV LKTAPLIHDGP SHVGIPRSCPKPLDKRQAHLVCLAS \NCDEPTMYVKLVEAL\CAEHQNP *LRVD\DNKKLG\EWG*GLLLKFDR GGGKPRKSWLG\CSCFS*FKDY\GK ESQAKDVIV\YFKCKK
1724	7221	A	1854	110	776	SLASGPYL\THQQKVLGLYKRALRH LE\SWCVQRDKYRYFACLMRARF\ EEHKK*KRIWAKATQL\KKEARGKN FWYPVKHPKSQYILPLTSPLGGHP Y*EDHD/CAYKVPRIGCL\DWHP E\KAMYP\DYFCORREQWKENLRR GKAWGTEGLSSLQE\ETPG\GP TESFAPWPEKEGD\LPPLW\WYIVT RPRERPMLERERPHLSCLQVKYVT EHGTCP

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1725	7222	A	1855	1	858	
1726	7223	A	1856	165	856	PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIW\FFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGKRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGP*NPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKC\REPLQCGFPGN LDPLSSILLGRREGIQMV\LCAN\QV\ VNGPPWGTLCGGTCQCCGCCGG\D GPVLNLRA
1727	7224	A	1857	163	1322	PGPYCGPVATMSLHGRRKEIYKYE APWTVYAMNWSVRPDKRFRWALG SFME\EHNNEGYLDGLDEERS*VI\ KNILDRPYPTNKVMWIPDTKGVYP DLLATSGDYLRVWRVGETETRL LLNNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDK\EVYDIAF SRAGGGGRDMF\ASVGADGSVRMFD LRHLEHSTIYEDPQHHPLLRLCWT KQDPNYLATMAM\DGMEVVILDV RVPCTPVARLNNHRACV\NGHLLW\ APHSS\CHI\CTAAG*PPGFSSWDI\Q QMPRA\IEDP\ILAYTAE\GEINNVO\ WA\SNSAPNWESPIC\YNNCPWRYS ECSVGGAVPHEAGAFVFPASAPPPK
1728	7225	A	1858	1	420	REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTLEEQ VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQRTYRGL* ILAKRAETVVDPEMTP
1729	7226	C	1859	28	156	MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPKPGLV*
1730	7227	A	1860	1	315	
1731	7228	A	1861	1	119	
1732	7229	A	1862	1	1477	
1733	7230	A	1863	3	1866	PLQSGHSAGRGGSGVAQGWHKKK YLQAKM\TKFLREERIQ\WKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPRLKK\DRKNLLET RLHITGRELRSKIAETFG\QENYIKI VINKKQLQLGKTLEEQGVVAHNVKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQRTKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKLNLAQKCFKNCYGENHQ RLVHIKGNCGKEKVLFLRLYLLQGI RNYHSGNDVEAYEYLNHRHVSSLKS YILIHQKWTICCSWGLLPKHLRLGL RACDGNVDHAATHITNRREELAQIR KEEKEKKRRRLENIRFLKGMGYST HAGQ\QILLSNPQMWWLNDSPET

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						DNRQESS\SQENIDRLVYMGFDALV \AEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEIIIAEYLSYVENRK SATKKN
1734	7231	A	1864	1	727	MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTLFPSSGGGGGAKAT AAAGAGLASPGMKTNGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPGQGWSSRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGATIEVF LPRLKKDRKNLLETRLHITGRELR SKIAETFGLQENYIKIVINKKQLQLG KTLEEQGVAHNVKA\M\VLELKQSE EDARKNFQL\QEEEQNEAKLIEERL QRTKRGL\AILAKRAA\EPVVVPEMT PYLDIANQTGRSIRPPSERKALMLA MGYHEKGRAFLKRKEYGIALPCLL\ DADKYFCECCRELLDVTVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKNCYGENHQRLVHIKGN GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLNHRHVSSLKSYILIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAATHITNRREELAQRKEEKEKK RRLENIRFLKGMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVA\EAALRVFRGKVPVAAQT PAYNGGSL\PFPELPLS\AEDSLSPAT \SPSDSAGT\SSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEIIIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQHQCLAP RFPVRLGTSPGQGWSSRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGATIEVFLLPRLK KDRKNLLETRLHITGRELRSKIAETF GLQENYIKIVINKKQLQLGKTLEEQ GVAHNVKADGCLN
1735	7232	A	1865	1	513	PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPRNLAAAVEE QYSCDYGSGRFFILCGLGGIISCGTT HT\ALVPLDLVKCRMKVDPQKYK GIFNGFSVTLKEDGVRLAKGWAP TFL\GYSMQGLLQVLAFYEVFKVLY
1736	7233	A	1866	2	1296	ALCEPQPFQSGSCVIALGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG TTHTALVPLDLVK\CRMQVDPQKY KG\IFNGFSVTLKEDGVRLAKGW APTFLGYSMQGLCKFGFYEVFKSL\ YSNMLGEVENTYL*RTSLYLAASAS\ AEFFADIALAPMEAARKVRIQTQPG

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						YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTVÆ A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSPLPEFLG*P VLD*GKKVSQCFLWVLQRDLGFK\ GV\WKGLFA\RIIMIGTLT\ALQWFI YYSVKGYFR\LPRPPPP\EMQES\LK KKLGVNSVVRIKANCGLNLLVDPV FEESAKGTFIYLTV
1737	7234	A	1867	127	433	RPLESWIGLVRCNICRSPIAEAVFRK LVTQDNISKNNWRVDSAATSGYEIG NPPDYRGQSCMKRHGIPMSHVARQ \DLNRKSNRVKTCCKAKIELLSYDP QKQL
1738	7235	A	1868	2	535	
1739	7236	A	1869	551	1299	PADPPRPSYYRHRTPPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVTQDNISKNNWEGRQGR NFRWVIDSGAVSDWNVGRSPDPRA V\SCLRNHGIHTAHKARQITKEVFP TFDYILCMDESNLARDLNRKSN\RVK TCKS*KFELPWEL*SPQKQLIED\PY YGE*LWTLETVYQQ\CVR\CCRAFL\ EKAH
1740	7237	A	1870	85	563	SSFLDIVHVCNTPNVKKMVGSGSSHK VIEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSETQIYLGWQV KIGFPNF*NPVAGILDRTKYRIFP*AP GIHKLKGYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK
1741	7238	C	1871	604	804	MKRLRLRLRXINNLAKITQPLSKTAL NLSPTQGGSKSRAILEFQLSRPGVNP PTLNWPSLNPFREPE*
1742	7239	A	1872	64	73	AFL*RWGSPCCPRAGLK/PP*P/PSI CPRPPPKPAGITRREPPGQAYFLII*F PSI*L
1743	7240	A	1873	47	225	NSHHVRGRPRCADSSSPSGDRGQPE AQPADSSAPEHAQEPGRAAVKRP DL*SHMTRRP
1744	7241	C	1874	101	232	MTMITPSSKLTLTGKNKSWSSSTAVA AALELVDPGGRNSARGF*
1745	7242	A	1875	66	723	AILIILLSSEGLWSSDQHRLVGVQDS PPQGLCCHFSAMATSEQSICQARA SVMVYDDTSKKWVPIKPG\QQGFSR INIYHNTASNTFRVVGKVFQDQV VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTFSNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFLERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPPVPPPTGA\TPPPPPPL\PAG GAQGSSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGGLMEEMNKLLAKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKAASQSDKPAEKKEDESQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAGPR KLRAFPSQQPHSRMKPAGS\VS DMA \LDAFDLD\RMKQEI*KEVVRELHK GERKEIID\AIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPLM
1746	7243	A	1876	1	668	GERGVARHDRPRGTLREYKVVGR LPTPK\CHTPPL\YR\MRIFAP*SMSSL SPRF\WYFVSQLKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRL\YDS RSG\THNMY\REY\RDLDHPQAPVHP SCLTRDNGVAPAPAA\HEAHFHFRI ERLEE\AGQQDCRRPGCSKQPRIS RFKFPAAPPGSLRRQDKPRF\TTKRP KTFLLKVQGPSSGVCPQNKTQETPR
1747	7244	A	1877	1	1059	
1748	7245	A	1878	87	260	
1749	7246	A	1879	1	1254	
1750	7247	A	1880	160	615	PSLNTYVTSPLSENFSAARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSV\IHTACIIDVFGVT HRESIMNVNVKGRVAWGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFSFIDEKTRT EQ
1751	7248	A	1881	53	1338	CPLQGHPRVTLESDDLPSIFCFLVSD SCYFGLATMGWSCLVTGAGGLLGQ RIVRLVVEEKELKEIRALDKAFRPEL REEFSKLQ\NK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIIQNG HEEEPLEN\TWPAPYPRSKKLA\KKA VLAANGWNLKINGGALYTALRPM YIYGEGSRFLSVSINEALNNNGILSS VGKFST\NVPVY\GNVAWGHLAL RALQDPKKAPSIRGQFYIISDDTPH QSYDNLNYTL\ASKE\FGPPPLDSRW\S FPLSLMYWIGFLLGNR*GFLLRPIY TYRPPFNRHISSHCSN*ALFHLLFIKE GFSEILGVLRLPLTAGGGKAKAGKR VGSWVWVPFVDPAQGRNLEVPRIQ
1752	7249	A	1882	3	575	HSLFGTSEVINKLLVPDA\MGHFTEE D\KATITSLWGK\VNVE\DAGGE\TP GKGSLLVVP\WTQRF\FDSFGNLSS ASA\MGKPPKSKAHG\KKVLTFLGT MPTKHLE*FSRGTFCPSLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP
1753	7250	A	1883	1	960	GRPAPEDGGPLSLPNAAMARGPKK HLKRVA\PKHWMLDKLTGVFAPR PSTGPHKLARECLPFIIFLRNRLKYA LTS\DEVKKICMQRFIK\IDGQVR\TD ITYPAGFMDV\ISIDKDGREFSVL/Y LIDTQGVRFCL*HRITP*GRAKVQSC AKMRKILLWAPKGIPSSWVTHDAR

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						NHPATPDPPSSKVN*YHFRLDLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITN\RRERHPGIF*PLVHV \DANGNKLLATSDFSNIFWLLGKGN KPW\ISL\PRGKGIPPHHLLLEERDKRL AAKQSSWVKWGPWVTWSDLLVP
1754	7251	A	1884	1	1218	FFQNSARGAGAGWQLPWTRFVWT SGLLEINE\TLVIQQRGVRIYDGEKI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQ\VFIEEQA\AGIGKSAKI VVHL\HPAPPNKEPGPFQSSKNSYI KLSFKEHGQIEFYRRLSEEMTQRRW ENMPVSQSLQTNRGPPGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHMAQLAKQL\AWNIA RVPLEERGIMSLETVYCLVNRARG MELLSPEDLVNACKMLEALKPLR LRVFDSGVMVIELQSHKEEEMVAS ALETVSEMGSLS*EFAKLVGMSVL LAKERLLLAEKMGHLCRDDSVGL RFYPNLFMTQS
1755	7252	C	1885	179	361	MPKVCVHNFCLKTSSERDLFALMN TVGKKHSHIMSEKGRSKKFLHLIDSK KNEDPHLDGTL*
1756	7253	A	1886	2	913	RRLLFGWARGAVSLGSAGVSSS GFLTAPHSRRLTAAAAAAGGAWRF EAERHRGWGAEEEQQPEGGA\CPG TERPCAMAYAYLFKYIIIGDTGGGR SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIK\QIWD\TAGQES FRSITR\SYRGAAGALLVYDITR DTSTHLTTWLEDA\QHSHFQHGS LCLLGKNSDL\ESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSCKNCFPM* KEAFINTSKRNFIKIQ\EGVFDINNE A\NGIKIGP\QHAATNATHAG\NQQG QQAGGGCC
1757	7254	A	1893	138	426	FIHSHCCIVFRLFIHFSLHPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFW*V YTFPF\GINPKKGIARL*GVYIFSFSIY CQTVFQSDCKKAPF
1758	7255	A	1894	45	1057	FLVFLVETGFHHVAQAVLELLASSD PPALAPKCDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFCSLSLS SWDYRCMPPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA\FPKC\W DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKTTSHLPTKEALT W/VSHATAKHLWILVSILMEF*VA LIS/SFLGPGGK*T*VTAPQCPSLGQ DTLS*FLHAACRSVPYPGLA/CGPS LWLTRVLLLPTPP*QQHNP/DTLEKT SFPGPWWIL*/TPQPSLSETPAPKVPP FPAFGSIPTHEEPLP
1759	7256	A	1895	2	289	

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1760	7257	A	1896	1	397	
1761	7258	A	1897	1	410	STMISPVLLFSSFLCHVAIAGRTCPK PDDLFPSTVVPLKTFYEPGEEITYSC KPGYVSRGGM\RKFCPLTGLWPIN TLKCTPRVCPFAGNLRKMGA VRLIT DFLNYSPTRFSSLLTWGFILEWAL DS\AKCIEGG
1762	7259	A	1898	19	1215	CQCDSSSTMIFSRCSLSSFLCHVAI AGRTCPKPDDLFPSTVVPLKTFYEP G\EEITYSCKPGYVSRGGIEESLSCPL \TGTVGPFNSTGNVTPRVCPF\AGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSC\TGKKGKWS P\ELPGLVAPI\CPP\PSIP\TG\ATLH VLLRPFRLGNNSPPIGDTAVFECLA HNAMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFPHQDPDNGIW*TYP CQNPNTLFTRVKAPHLGLPHDGIFS GMGPRKE\EC*PQ\TWGKPGSWPLA PSW*KPSLVKGTVPVKRPTVV\YPQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\DA\DVKPC
1763	7260	A	1899	58	446	
1764	7261	A	1900	1	954	MGEVSGTSDCTDDQCRQVKKALEG GKAARGHRSKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA V\ERLLNGHAKILEVDLKNYGFVE FDDLRLDADDAVYELNGKDLGGERV IVEHARGPRRDGSYGSGRSGYGYR RSGRDKYGPPTRTEDRLIVEN\LTSR CSWQDLKDYMROAGEV\TYADAHK GRQKMKGVIEFVSYSMDKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRSRHSRKSRSRSGSS KSSHSKSRSRSRSGSRSRSKSRSRSQ SRSRSKKEKSRSPSKDKS\RSRSHSA\ GKSRSKSKDQAE\EFQ\NDNV\GK PKSRSPSRHKS\SKSRSRSQERRVEE GRKRGSF*QGQ\EAQEKSLRQSRSR\ SRSKAGSR*PVDRSRSKSKDKRKS KRSREESRSRSRSRSKSERSRKRGS KRDSKAS\SKKKKKEDTDRSQSR PSRSV\SKEREHA\RSLESSQREGRG ESENAGTNQEDPGPGPRSN\SKSKP NLPIRMHRSKIKSQASKTPISGPMSR SR\SASRSP\SRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP
1765	7262	A	1901	3	180	
1766	7263	A	1902	227	440	GMHNV\CYVAVNE*FCGFIIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMASPVAGSWSHFPEREF
1767	7264	A	1903	2	438	HEELDTSERKIEFDSASGTYTLYLN GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLFTPK\QEIQWIRI GA\NVSNFTFAP\STIIFH\LGHA\AM LGLMYVYWTQLNMF\QTLKYLAIL GSVTFLAGNRMLAQQAVKRTAH

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1768	7265	A	1904	1	1660	
1769	7266	A	1905	156	2369	PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFGRLRRDLLGGMAPP SSTVFLALTIHASTWALTPTHYLT HDVERLKASLDRPFTNLESAFYISIV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYA\AQASQGLSGCEISIN ETKDLLLA\AVSE\DSSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQGGKTVL\ATVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQ\FEEGLETTALFVAATYKA /LMDH\VGTE\PSIKE\DQVIQLMNAI F\SKKNFES\LSEAFSV\ASG\AAVLS HNRYHVPVVVVPEGSASDTHEQAI LRLQVTNVL SQPLTQATVKLEHAK SVASRATVLQKTSFTP\VGIVFELNF MNVKFSGG*CDF\LVEVEGDNRYIS\ NTVELRVQDPPTVEGITNVDLSTV\ DKDQSIAP\QTRVTYPKAKGTFH SAGQATRNFGLVLSSW*DVNTGVAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSERKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVVKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPPWCP NTFTAPESFFGPLL/LCFLRLWIRD WVPKCLPTFTFCFLSTIIFHPWDML AYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH
1770	7267	A	1906	37	404	PQLSRCRSECMYVNPTVVM TSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHEVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1771	7268	A	1907	271	1086	YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAAVALLQPFLEV TKEAFDR*ACEGGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVA\RGLIARGVPTGPS*NVSSQC FPAGQ*TNHSVLLLP TKGVPLDMLD QG*WAL\ELGPHKLSRCRSGVNA\V NPHSGG*RSMGPGPPWSDPHK\AKI MLNRIPLGKFAGESEVEHVVNAIL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT
1772	7269	A	1908	2	305	ARESGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHE\ECMPLYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A
1773	7270	A	1909	2	529	GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSEN FYSVFEGELSDTIPVVHASIAGCRIIG RMCVG\TEEILADV LKVEVFRQTV DQVLVGSYCVFSNQGLVHPKTSIE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DQDELSSLLQVPLVAGTVNRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE
1774	7271	A	1910	18	889	GVQGTVAACGACYWLLGLMAVRA SFENN\CEIGCFAKLNTYCLVAIGG SENFYSVFEGELSDTIPVVHASIAG CRI\GRMCVGN\RHGLL\VPNNTTD Q\EL\QHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWEVFRQ TV\ADQV\LVES\YCVFSNPGRAWVP SPRPFQ*RPRNELSSISFKVPL\VAGT C*TKGSEVICLLGMGGEMNWCA\FC GPGTPNPAQSCQVVEECLQS*NEAP ALAPIANRACGNSL\IDSLT
1775	7272	A	1911	132	440	
1776	7273	A	1912	149	389	FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYN\YNVLMVPKPQGGLP NTALLSLVLMAGTFFFAMMLRKF NNS
1777	7274	A	1913	3	153	
1778	7275	A	1914	94	593	LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYN\YNVLMVPKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKN SYFPGKLRRVIGDFGVPICLIMVLV DFFIQDTYTQKLSVPDGFKVSNS RGWV\HPLGLRSEFP\IWMMFASAL PALLVFILIFLESQITT
1779	7276	A	1915	115	3015	TTGHSGPRHGAAGGCSLASAVLP PGGSGDLVLD\SYLRWGWSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPA\AHDTEATADYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAA\PLR\QLDENLG\ENGAW GRPHLSHLTFWSLLELRRVFTKGT VLLDLQETSLAGVANQLLDRFIFEDQ IRPQDREELLRALLLKHSHAGELEAL GGVKPAVLTRSGDPSQPLLQHSSL ETQLFCEQGDGGTEGHSPSGILEKSP PDSEATLVLVGRADFLEQPVLGFR VRLQEA\AELEAVELPVPIRFLFVLLGPE APHIDYTQLGRAAATLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDDPL QQTGQLFGGLVRDIRRRYPYLSDI TDAFSPQVLA\AVIFIYFAALSPAITF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL\VGFSGLLVFEE AFFSFCETNGL\EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFIS\RYTQ EIFSFLIS\LIFIYETFSKLIKIFQDHPL QKTYN\YNVLMVPKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGVPI\ILIMVLV\DF FIQDTYTQKTSQVPDGFKVSNSARG WVIHPLGLRSEFP\IWMMFASAL\PC LLVFILIFLESQITTLIVSKPERKMKV

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						GSGFHLDLLLVVGMGGVAALFGMP WLSATTVRSVTHANALTVMGKAST PGAA\AQIQEVK\EQRISGLLVAVLV GLSILMEPILSRIPLA\VLFGIFLYMGV TSLSGIQLFDRILLFKPPKYHPDVP YVKRVKTWRMHLFTGIQIICLAVL WVVKSTPASLALPFVLILTVPLRRV LLPLIFRNVELQCLDADDAKATFDE EEGRDEYDEVAMPV
1780	7277	C	1916	20	202	MAAIKYLGISAILYYKYKCPRGQGN QPEELGTGSILCGNFSGLMFLFPVQM YTVKKA YRAV*
1781	7278	A	1917	1	493	
1782	7279	A	1918	214	612	
1783	7280	A	1919	287	847	SDRPTMAPGVARGPTPYWRLRLG GAALLLLLIPVAAAQEPPGAACSN TNKTCEECLKNVSLWCNTNKACL DYPDTSVLPPASLCKLSSARWGV WVNFDAIITMSVVGTTLLGIANC CCCCRRKRSRKPDRSEEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\ YGLFKEENPYARFENN
1784	7281	A	1920	61	515	
1785	7282	A	1921	1	2175	
1786	7283	A	1922	3159	3441	
1787	7284	A	1923	36	387	
1788	7285	A	1924	64	408	
1789	7286	A	1925	1	10514	
1790	7287	A	1926	64	601	VNNILGLGHTFWALLASPKMEHKE VVLLLLFLKSGQGEPLDDYVNTQ GPSLFSVTKKQLGAGSREECAAKCE EDKEFPAGAF\QYHSKEQQCVIMA ENRKSS\INRVRDA\VLFGKGKCILF RVQDLGMERTTEGRCPKQKMASPC QKWEFHFSPADLGQTFPFIFVFIYCK VVPLCL
1791	7288	A	1927	173	491	AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQQVWREPPGPASK APHSPPVGYSSPGHESHLPGDDPA KDGSCPPI\PFPLGIEAPVPGPRKRIR TCCCMN
1792	7289	A	1928	1	735	
1793	7290	B	1929	1	1026	MRARRLPWALT\VAELGWDTQGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVFLLLWPFSSSTLAKHKRIHTGE KPYKCEECGKA\FSRSSTLAKHKRIH TGEKPYKCKEKGKAFRQSSTLTKH KIIHTEEKPYKCKECDKAFKRLSTL AKHKIIHAGEKLYKCEECGKAFNRS SNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKA\FSRSSTLTKHKTIHTGEKPY KCKEKGKLLSTPQPLLNK*
1794	7291	A	1930	1	2832	

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1795	7292	A	1931	98	3867	PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQNLYR NVMLENYRNLAFLGIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLLRKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKVFQCGKYL KVIFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TQHKCVYITEKSC KCKECEKTLW\SSTLTNHNKIEHTED KPYKCEECGKAFAKQLSTLTTHKIIC AKEKIYKCEECGKAFLWSSTLTRHK RIHTGEKPYKCEECGKAFFSHSSTLA KHKRIHTGEKPYKCEECGKAFFSHS ALAKHKRIHTGEKPYKCKEKGKAF SNSSTLANHKITHTEEPYKCKECD KTFKRLSTLTCHKIHHAGEKLYKCE ECGKAFFNRSSNLTIHKFIHTGEKPY KCEECGKAFFNWSSLTCHKRFRHTR EKPFKCKEKGKGFWSSTLTRHKRI HTGEKPYKCEECGKAFFRQSSTLTCH KIIHTGEKPYKFEECGKAFFRQSSTLT CHKIHHREKPYKCKEKGKAFKQFS TLTTHKIHHAGKKLYKCEECGKAFF HSSSLSTHKIHTGEKSYKCEECGKA FLWSSTLRRHKRIHTGEKPYKCE CGKAFFSHS\ALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTCHKIHH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFNWSSLT CHKRIHTREKPFKCKEKGKAFIWS TLTRHKRIHTGEKPYKCEECGKAFF RSSTLTCHKTIHTGEKPYKCKEKGK AFKHSSALAKHKIHHAGEKLYKCEE CGKAFFNQSSNLTTHKIHTKEKPSKS EECDKAFFWSSTLTEHKRIHTREK PYKCEECGKAFFSQPSHLTTHKRMHT GEKPYKCEECGKAFFSQSSTLTTHKII HTGEKPYKCEECGKAFFRKSSTLTEH KIIHTGEKPYKCEECGKAFFSQSSTLT RHRMHTGEKPYKCEECGKAFFNR SKLTTHKIHTGEKPYKCEECGKAFF SSSTLNGHKRIHTREKPYKCEGCG\ KAFFSQSFN/TLTGHKRLHTGEKPYK CGECGKAFFKESALTCHKIHTGEK PYKCEKCKAFFNQSSILTNNHKIHT ITPKIHTREKPYKYKECGKSFNRSS FTCHKVIHTGVKLYKCEECGKSFF WSSALTRHKIHTGQQPYKQEKFG KAFFNQFSLTTR
1796	7293	A	1932	590	891	
1797	7294	A	1933	1	1527	
1798	7295	A	1934	13	1668	PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFL\GPHLVQSDGTVPFWA HAG\AISSSDQIRVAPSLKSQRGSV WTKTK\AAFENWEVEVTRVTGRG

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						RIGADGLAIWYAENQGLEGPVFGS ADLWNGVGIFDSDNDGKKNNPA IVIIGNNGQIHVDHONDGASQALAS CQRDFRNKPYPV\RAKITY\YQNTL\ TVMINNG\FTPDKNDYEFCAKVEN MIIPAQGYFGISAATGGLADDHDVL SFLTQFQLETPGKEPPTPDKEISEKEK EKYQEEFEHFQQELDKKKEEFQKG HP\DL\QWQPAEEIFESVRD\RELRLQ VFEGQNRHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRGAGMPGQHG QITQQELDTVVKTQHEILRQVNEM KNSMS\EPVRLVSGMQHPGSAAGGV YG\TTQHFID\KEHLH\VKR\ DIDNL VQRNMP\SNEKPKCELPFPSPCLST VHFQIFVVVQTV\LFYGYMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV
1799	7296	C	1935	238	360	MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGPL*
1800	7297	A	1936	1	1656	
1801	7298	A	1937	83	260	
1802	7299	A	1938	1	678	
1803	7300	A	1939	1	1097	
1804	7301	A	1940	1	1706	MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSSRLDSLKRDIYAGKPQPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWPCIME TLNASGTFAIRLLKILCQDNPSHN FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLTEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIYFKGKWNEPDET YTREMPFKINQEEQRPVQMMYQE ATFKLA\HVGGLRAQLLE\LPYARK ELSL\ VLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFVE VNEEGTEAAAASSL\WVVAECCME SGPRFCADHPFLFFIRHDRANSILFC GRFSSP
1805	7302	A	1941	3	428	ETLERIKNNDPKLEEVNLNNIRKIPI TLKAYAEALKENSIVKKFSIVGTRS NDPVAYALAEMLENKELKTLNVE SNFISGAGILRPGEALPYNTYLVEM RSDNQSQPPGNKVEMEIVSML\EKN ATLLRVR*HFSQQDAR
1806	7303	A	1942	1	1258	ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQETQTS SSTMSYRRELEKYRDLDEDEILGAL TEEELRTLLENELDELDPDNALLPAG

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						LRQKDQTTKAPTGPFFKREELLDHLE KQAKEFKDREDLVPYTGEKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSIMNKEGLNSVIKPTQ YKVPVDEEPNSTDVEETLERIKNND PKLEEVLNNIRNIPIPTLKAYAEAL KENSYVKKFSIVGTRSGDGVAYAL AEMLKENVLKTNLVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHFLKFGL PPYPSKEPRLR\ASTAMMTIALVR E\RRLLAAPDLGPSFPKCRSGV
1807	7304	A	1943	2	382	EIAHQIEQQMG/EG*NFVAIESVV*K IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTTPDAAGVNQ\LFFTTPLDSAQ HLQDVIMGAVTCEGCKGFFKRSIRK N
1808	7305	A	1944	240	454	
1809	7306	A	1945	1	1851	
1810	7307	A	1946	128	512	TAPLAAGRPRGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYRRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL
1811	7308	A	1947	1	705	
1812	7309	A	1948	124	1583	IMATIEEIAHQIEQQMGIEIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTTPD AAGVNQ\LFFTTPLDSAQHLQLLTD NSPDQGPKNVFDLCVVC GDKASGR HYGAVTCEGCKGFFKRSIRKNLVYS CRGSKD\CIINKHHRNRCQYCR LQR CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLD SGFMFNIHPSG VKTESAVLMTSDKAESCQGD LSTL ANVVTSLANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDTLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLS SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALG\QEK QP*SLVKAYWNEFLTLGLAQCWQV MNVATILATFVNCLHNSLQQDAKV IAALIHFTTRAITDL
1813	7310	A	1949	6	2028	KILRTLTPQYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRGSRGTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGIEIVTEQQTGQKIQIVTALD HKTQGKQVILTNDHGSTPSKVILAR QDSTPGKVFLTTPDAAGVNQ\LFFTT PDLQAHLQLLTDNSPDQGPKNV DLCVVC GDKASGRHYGAVTCEGC KGFFKRSIRKNLVYSCRGSKD CIIN KHHRNRCKYCR LQRCIAFGMRQDS

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						VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDLSLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNGDVSRAFDLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTD\KEGPLLSDSHVAFRLTMP SPMPEYLVNHYIGESASRLLFLSMH WALSIPSFQGSRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILA\TF VNCLHNSLQQDKMSTDRRKLLME HIFKLQEFNCNSMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTYPDD\TYRLSRLLL RLPALRLDGCT\NTEELFFKGLIGNIR IDSVIP\HILKMEPADYNSPIHHSI
1814	7311	C	1950	65	286	MDYCNFTLPSNPETVFGDIMPRVVK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIYP*
1815	7312	A	1951	15	82	
1816	7313	A	1952	2	1934	CVQAATSLSVGICPLPGPGSPPPWY PGVSVNVWIFKQIDDEGDLRLINK EVLSGVVVVISSKDSVQHGVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQOEG SEEAGGLSGAEALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGKVLVYETYHGVFVNIQYTLRC DMKRSLAKDLTKTCEFIVHSAPQK GKFTPSPVDFTTITPETLQNVKEHSQ TEAGQQRAFRFRSALRGGRLTAR ADNSSSSNVAQGSQKSGHPCSRPSS VLPGRQVCRVKRALLPKFLL\RRT SQLNKLCHHAATNGRAGGGELGSR HQKRGAAAGARGDPGQQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCR\SYARDATEIQNIQIADGDVCR GLSVPIYMFVPRFLTCTPTLETTFKV GKWHSPSPHGPMPGAAQRQGLL WVTELRTCRPSVPQCQGLPQAIQLR ACCPAAQQNLVKELLCRTGDTPT GSPGACGTSTVTWGNTQTHISVDM GRPQPQVGTDSKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQQGSPIAEESVEKESCLLK EFEVNIVVLLHPDHLITENFLKLCR I
1817	7314	A	1953	262	1274	ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMTGLDIKSKR ANKVYHAGEVLSGVVVVISSKDSVQ HGVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFPS GKTEIPFEFPLHLKGKVLVYETYHG VFV\NIQYTLRC\DMKRSLAKDLT KTCEFIVHSAPQKGKFTPSPVDFTTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK

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						RGAAAGARGDVRVCR\SYARDAP/E IQNI\QIADGDVCRGLSVPIYMFPR LFTCPTLETTNFKVEFEVNIVVLLHP DHLITENFPLKLCRI
1818	7315	A	1954	2	236	DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQPRVPPPRSSM S
1819	7316	A	1955	760	925	HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRRGRITGGQEFKTSVANIT KPCLY
1820	7317	A	1956	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1821	7318	A	1957	41	638	APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEKCWKEKTPGKGSLLVYP\ WT\QRFFD\SFGNLSSAF\AHHGQTP KVKAHGK\KVLTFLGRCQQSTLDD LKGTFAQL\SELHCDKLHVDPENFK LLG\NVLVTVL\AIHF\GKDFTPGGC RASW\QKMGD*SGQCPVLQIPLSS LPMMQSFSRIRLLFLQAITNNKSISA KRSP
1822	7319	A	1958	3	227	
1823	7320	C	1959	171	366	MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEDVPLYPEW CMLWRYPASRPNVKRP*
1824	7321	C	1960	332	421	MEEKIFSQPGMVAPT CNPSTLGGQG RWIT*
1825	7322	A	1961	322	1145	RFSKSPDSDGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRAASADSSLPG CGRREVCGSRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEAADDSYGVA GRWGRPVQDSRLGTAGEGIAGRES WGSVTSWVLGSHMVKFGFLVAELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML
1826	7323	A	1962	30	2814	LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSRSPLDPEM ARPRRAREPLLVALPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQGVHRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALS FVQALIRGRG DGDEVGVRCPGGVPPLRPAPPERV VAVVGASASSVSIMVANVLRFLAIP QISYASTAPELSDS\TRYDFFSRVVP DSYQAQA\MVDIVRALGWNVYSTL ASEGNYGESGVEAFVQISREAGGVC

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						IAQSIKIPREP KPGFSK VIRRLMETP NARGIIIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAITILPKRASIDGFDQYFMTRSL ENNRNRNIWFAEFWEENFNCKLTSSG TQSDDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIHAHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDA PGRY DIFQYQATNGSASSGGYQAVGQWA ETLRDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCWHCEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPLL LAVLGIVATTTVVATFVRNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGA AVCAARRLFLGLGTTLSYSA LLTKTNRIYRIFEQ GKRSVTPPPFISP TSQLVITFSLTSLQVVGMI AWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDLSLIGCLGYSLLMVTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGT AQSAEKIYIQTTLT VSLSLSASVSLGMLYVPKTYVILFH PEQNVQKRKRS LKATSTVAAPPKG EDAEAHK
1827	7324	C	1963	334	387	MKCYIYIYMTLVLLIV*
1828	7325	A	1964	1	489	
1829	7326	A	1965	152	717	VESIEDVGNHRTDHGADMISIH YEE ENAFILDTLAKKQWKGPDDILLGMV YDTD DASFKWVDNSNMFTDKWTD QDDE\EDLVDT\CAFLHIKTGEWKK GNCEVSSVEGTLC KTAIPYKRK YLS DNHILISALVIAS TVILTVLGAIIWFL YKKHSDSRFTTVFLTGPQLPYMEN CVLVVGEENEYYPVQFD
1830	7327	A	1966	3	614	LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCYAYL QMKGNR\EM\YDCTSSSFDGIAM MSPED\SWVSK\WQAKSSNFKP\GV YA\SVVTGRLAPKGIR/VRELKSRIG VALQIPGDTANKDLAKMQGCQHLC SPPPCLCIISCSWNLNEQNFQILPTLQ FRLSSTVERAAHHFI LSSLDYRWG GRDLGWVD
1831	7328	A	1967	66	407	
1832	7329	A	1968	2	1272	CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRGVEHGPAAIREAGLM KRLSS/LGDLTSP EIEVLFTDI AKVR THCPKSLPGTETVQIELSSFFLNILG GKKKKQSWEQEGCHLKDFGDL SFT PVPKDDLYNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDLCVVWVDAHAD I NTPLTTSSGNLHGQPV SFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVPPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPIHLSF

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						DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI
1833	7330	A	1969	212	460	
1834	7331	A	1970	1	1223	TVVECLSPA WHEESSGGRWRSRPA SNRAEPLPWRFSVLRLMSLRGSLSR LL/QTRVRSILKKS VHSVHVIGAPFS QGQKRKGVEHGPAAREAGLMKRL SSLGCHLKDF/GQDLSFTVPVKDDL YNNLIVNPRSVG\LANQELAEVVSR AV/SQDGYSCVTLG DQSLAIGTISG HARHCPDLCVVWVDAHADINTPLT TSSGNLHGQPVSFLLRELQ/DKVPQ LPGFSWD/IKPCISSARIVYIGLRDVY PPEHFILKGTMDIQYFMSMEEILDR\I GIQEGHNGTDFD\LIGKRQRPIH\LS YDIDAFDPT HAPAHRT/PVVGDITYR EAMYIAEKIH\NTG\LLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTREGGAYWSYDPTFTPTASSP\ DESENQARVRI
1835	7332	C	1971	162	425	MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVGNIGRQLAMGVPEK PIVIESSKPXILESXGRFLEENLXLVD YXKGLSFFLK*
1836	7333	A	1972	89	308	
1837	7334	A	1973	2	454	
1838	7335	A	1974	570	1418	PMPRLHDHFWSCSCAHSARRRGPP RAIAAGLAAKVGEMHIVFVSGPSLM AVLSASDADPAPGRSAVKSGPYP GSPYPNTWHHSLMQKSLVLFVGE VLALVLNLLQIQRNVTLPFEEVIATI FSSAWWVPP\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGOVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSLGLGNTIAFL ATL\ITQFLVYNGVYQYTSPDFLYIR SWLPC\IFFSGSVTVGNIGRQLGYG VFLEKPHSD
1839	7336	A	1975	1	287	KFQERGHIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQTP/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSPKEKDV RPATSTTSCSMILLSILFIG
1840	7337	A	1976	1	166	
1841	7338	A	1977	37	448	GGCTCPCSRWQGSPPQAPAGLPPPL ASGPAPSASASPQSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPVLGPACESPGRGWV ASPWSSGWSP
1842	7339	A	1978	45	249	
1843	7340	A	1979	77	3801	KGGVFAHDLVPLPFQGTDSPPRAP PGRGVPLPPGALTMNTRD\TPRVAE TSHHLKIFLPKLLLECLPRCPLLPE RLRWNTNEEIASYLITFEKHDEWLS

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						CAPKTRPQNGSIILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLVQ GMECLYGCYVHSSIVPTFHRRCYW LLQNPDIIVLVHYLNVPALDCGKG CSPIFCSISSDRREWLKWSREELLGQ LKPMFHGIKWSCGNGTEEFSVEHL VQQILDTHPTKPAPRTHACLCSGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPELPKA HTSPSSSSSSSSGFAEPLERPSPTS RGGSSRGGTAILLTGLEQRAGGLT PTRHLAPQADPRPSMSLAVVVGTEP SAPPAPPSPAFDPDRFLNSPQRGQTY GGGQGVSPDFPEAAEAHTPCSALEP AAALEPQAAARGPPPQSVAGGRRG NCFFIQDDDSGEELKGHGAAPPISP PPSPPPSPAPLEPSSRVGRGEALFGG PVGASELEPFSLSFPDLMGELISDE APSIPATPQLSPALSTITDFSEWSY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLRCYCPAHEV GLVSLQVAGREGPLSASVLFYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQGGPFEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDPLNVDHFCTPLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRPLPSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPSSSPDTGLSSVS SPSELSDGTFSVTSAYSSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSSTPPSELPFERGRLAVPSA PSWAEFLSASTSGKMESDFALLTLS DHEQRELYEAARVIQTAFRKYKGR RLKEQQEVAAAVIQRKYRKYKQLT WIALKFALYKKMTQAAILQSKFRS YYEQKRFQQRRAAVLIQQHYRSY RRRPGPPHRTSATLPARNKGSFLT KQDQAARKIMRFLRRCRHRMRELK QNQELEGLPQPLAT
1844	7341	A	1980	1	4333	MQVQDDGVNLIPFAKCSRVVSRSP PRLPSQSLRPMPPQRYGDVFWKNLN QRPTPTWLEEQHIPPMLRATGCSQL GLYPPEQLPPPEMLWRRKKRRPCLE GMQQQGLGGVPARVRAVTYHLED LRRRQSIINDTDSPPRPLRPGVTLPP GALTMNTKDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPQNG SIILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLVQGMCECLYGCY VHSSIVPTFHRRCYWLLQNPDIIVLV

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						HYLNVPALED CGKGCSPIFCSISSDR REWLKWSREEL LGQLKPMFHGIKW SCGNGTEEF SVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLTSIPHAHPPE PPPLIAPLPPEL PKAHTSPSSSSSSSS GFAEPLEIRPSPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPQRGQTYGGGQGVSPDFPE AEAHTPCSALEPAAALEPQAAAR GPPPQSVAGGRRGNCFIQQDDDSGE ELKGHGAAPPISPPSPSPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTPQLSP ALSTITDFSPEWSYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGPERLAHGSPFR GMSLLHLAAAQGYARLIETLSQWR SVETGSLDLEQEVDP LNVDHFSCPT LMWACALGHLEAAVLLFRWNRQ ALSNPDSLGRPLSV AHSRGHVRLA RCLEELQRQEPSVEPPFALSPSSSSP DTGLSSVSSPSELTDGTF SVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQIHEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYL\ENVDFPSSTPPSEL\PFER \GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTL\SD\QE QRELYEAARVI QTAFRKYKGRR LKEQQEVAAAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYYEQKR FQQSRRAAVLIQGH YRSYRRRPGPPHRTSATLPARNKGS FLTKKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS
1845	7342	A	1982	1	145	
1846	7343	A	1983	1	419	
1847	7344	A	1984	3	532	PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTLLLNNEGSLLA\YS GLRGTTDAPGSPA AIA\SNIWA\AYG PETGTQAFNEDNLQI\ILHGTCTMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS
1848	7345	A	1985	2	555	
1849	7346	A	1986	90	323	

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1850	7347	A	1987	1	4695	
1851	7348	A	1988	81	523	SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFFSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\R SSDSWEVWGLASTNR\NSNSDGV GGEGTKKAVPPAVPTDDGWDNQNW
1852	7349	A	1989	1187	1720	QNQSRDKM\RDRLREGQMEPPKSELI GW\GGGETSRWVRGGASPPP\ALSP LFLITWSGHKDLK\DLKVRGLRGLE APRVNVWETEANQAGLQPLGPPAT IGLRPRERPGPGRVREGGPAWPLG EFGIPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGQPGQPAGPADG RAARSRG
1853	7350	A	1990	738	1086	GTASENLGCKILKHRQQMLRKVYP VVLHILSYRGSHSSRKKNWGRLEKNI LKTFFFLGGGGDGSCWQRPGWELQ WALFSGSLQSPPGFKQFSCSLLS SWEYRCTPPCLANFCIFQ
1854	7351	A	1991	1	340	LGEGGRTAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLRGRSLPKA WPPPPSSLPVLTDEQKS/YPGHEAH DQGG\WDARQSIIRKVDPETGRTR WGAFLTYTTGSGSVG
1855	7352	A	1992	1	142	
1856	7353	A	1993	58	328	LKKKGKEKAEAAQVEALPGPSLDQ WHRSAEEEEGPVLTDEQKS/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLKGDGEGPKRKS
1857	7354	A	1994	120	416	LFFGESSRLTVLEDLKNVFPQVAV FEPKAEIFHTQKAPLVFLATGFYPD HVELSWVWNGKEVHSGVSTDPQP LMEQAALNDSRYCLSSRLRVSATF
1858	7355	A	1995	1	977	VKLPSCPDPAMGTSLLCWMALELL GADHADTGVSQNP RHNITKRQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLLSDRFSAER PKGSFSTLEIQRTEQGDSAMYL CAS SIGAGLPSSNQPHFGDGTLSILED LNKVFPPEVAVFEPSEAEISHTQKAT LVCLATGIFPDHVELSWVWNGKEV HSGVSTDPQPLKEQPALNDSRYCLS SRLRVSATFWQNP RNHFRCQVQFY GLSENDEWTQDRAKPVTVIVSAEA WGRADCGFTSVSYQQGVLSATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF
1859	7356	A	1996	2	883	FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICQRGTSV KIECRSLDFQATTMFYWRQFPKKS MLMATSNEGSKATYEQGVKDKFL INHASLTLSTLTVTSAHPEDSSFYICS ARESTSDPKNEYFGP\GTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATG\FFPDHVELSWVWNG

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						KEAHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSATFW\QNPRNHFRQV QFYGLSENDEWTQDRAKPVTQIVS AEA WGRAGEWGLGRCLLEEIR
1860	7357	A	1997	195	1133	PQHGGHFPRKIKSCSWQARPLEDEA TLGQCGVEALTTLEVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEA VVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSSPYIEYT PASPAYAQYPPATYDQYPY\AASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH
1861	7358	B	1998	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
1862	7359	A	1999	1	437	DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDS
1863	7360	A	2000	2290	2481	
1864	7361	A	2001	3	860	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLP\PRPKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAG\TAA DTAMT\TQLISS\NLKLHSL\STGR\LP RV\VTANRMLKQMLFRYQGYIGAA LV LGGVDVTGPHLYSIYPHGSTDK VP\YVTHGFLAPLAAMAVF\EDKFR P\D\MEEEEA\KNLVSEDSPPQFP WRIFND\LGSGSNIDLCVISKNKLDL LRP\YTVPNKKGTRLGWRYRCEKG \TTAVLTEKIPLLWST
1865	7362	A	2002	1	340	RQGTIVAISSIQGKMSIPFRSAYAAS KHATQAFFDCLRAEME QYEIEVTVI SPGRSC/VEVAQDVLAAAGKKKKD VILADLLPSLAVYLRTLAPGLFFSL MASRAR*ERKSKNS
1866	7363	A	2003	56	385	RPWTSSPPQSPCCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLA AVGKKKKDVI LADLLPSLAVYLRTLAPGLFFSLMA SRARKERKSKNS
1867	7364	A	2004	2	409	
1868	7365	A	2005	1	1092	
1869	7366	A	2006	50	1101	LTMVSPATMKSLPKVKAMDFIT\ST AIL\PLLFGCLGV\FGL\FRLLQWV\R GKAYLRNAV VVITGATSGLGKECA KVFYAAGAKLVLCGRNGGALEELI\

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						RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNNAGISYRGTTMDT\TVVDKR VMETNYFGPVALTKALLPSMIKRR QGHIVAIISSIQGKMSIPFRSGICQPS KHATQ\AFFDCLAVPEMEQY\IEIV TVISPG\YIHTNLS\VNAITADGSRYG V\MDTT\TSPGPESPVEGGPRMFLAC LWGKKK\KDV\TLADLPALPLAVY\ LRTLAP\GLLPSSLPCLPRAQKRAGN PKNSLV
1870	7367	A	2007	75	461	
1871	7368	A	2008	3	426	DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYDLA GGAGPIDAEKGGSLVVGDFEIA TKY VCRTLETQSQSSPFSCMDLTYVSL LQEVGFPRSKVLKLTRKIDNVYTT WAPGAIFHYIDSLNRQKS
1872	7369	A	2009	3	421	QALGNRGVVSRGWRPGWRRPGRG SPKDRLPAPRKRALVSVGVAERA VHETPTLTHETFKALKPGLSAYADD VEKSAQGIRELLDVAQDIPDF*K ATPLILK\ATAGLRLLEKKAQR*LA \KGKEVFKAWLFFEGNDW
1873	7370	A	2010	337	769	PLALCLAPAAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYDLA AGVGLIDAEKGGSLVVGDFEIAAK Y\VGVTWSVKGRVSSPVCRTLETQP QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLTRKIDNVETSWALGAIF
1874	7371	A	2011	2	486	
1875	7372	A	2012	176	1643	MKKGIRYETSRKTNIFYQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVFIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFY GIMFDAGSTGTRVHVFQF TRPPRETPTL\TAHETFKALKPGLSA YADDVEKSAQGIRELLDVAQDIPF DFWKATPLVLKATAGLRLLPGEKA QKLLQKVKEVFKASPLVGDDCVSI MNGTNE\GVSAWITINFLTGLSKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KDGGELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHVDFYAFSYY\YD LAAGV\GLIDA\EKGGSLVVGDFEI AAKYV\CVRTLGETQP\QSSPFSCMD LTYVSLLLQEFGFPRSKVLKLTRKID NVETSWALGAIFHYIDSLNRQKSPA S
1876	7373	A	2013	21	119	PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK
1877	7374	A	2014	1420	1627	IGLNPSSVPSTFFSYSPQFTEGVPP/P GMERP/PFPWEQRPTGWSFFSPCPQ TP\SPPTSEHGTPPNWPKC

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1878	7375	A	2015	447	775	QIPKEHLHHP/PQTSNSRPLR/P/GN RPNPESPTGSPPECCSCLAPRGSA WGDPNPLQRTPGAGKVAGGPFPPP TQQSPPGKALCINLKKGFAAIKLLD NVLQPSSALGFL
1879	7376	C	2016	49	519	MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLSEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPFM SPRYPGGPRPPLRIPNQUALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTPPRGMVP*
1880	7377	A	2017	1	1155	
1881	7378	A	2018	56	1416	WVDRCVTVGAALGTSMYKGK\KS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLSEIRWEK\NITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEH\SSEAKAFHDYSAAAA\PSP VLG\NIPPGRWACQLGPVTTGRSFQ PFMFTFGYPG\GPRSPLR\VPNQALG G\VPGGQPLLPSGMDSTRQQ\GHPN MGGAMQR\MTPPRGM\VPPLGPQFLT PWLSLQNYGGAMRPPLNALGGPG MPGMEQGSRCGRPW\PNPTNA\NSL PFSSAFSWNLLGPPG\GGGPPG\TP\N MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNF\PMGP\GSDGPMGGLGG MESHMMNGSLGS\GDMAISIKNSPN N\MSLSIQP\GIPK\DDGAMGANFLN PFQSESYSPSKPYKCVFPFGLFMKP TVSQPFPELRTEENYSSTSVPVKQR NLSTKPTFLFPALSPLL
1882	7379	B	2019	162	349	LEEEEEEEELDLVLLRAFCLLLSW DVEAEQFLEVSFLLFFFLFSDPRPRD RLRLRLREPT*
1883	7380	A	2020	2	353	SSSDGRKKRGKYKDKRRKKKKKKR KKLKKKGKEKAEAQQVEALPGPSL DQWHRSAEEEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKV DPETGRTRWGAFLTYTTGSGSVG
1884	7381	A	2021	1	142	
1885	7382	A	2022	404	946	PVCACPRPEQGTKVYLFPSWLSLT FSLHHREKQAEGRGEEEDASSASS SSSSSSSSSSSSSSSDGRKKRGK YDKRRKKKKKKRKKLKKKGKEKA EAQQVEALPGPSLDQWHRSAEEEE DGPVLTDEQKSR/YPGHE\THDQGG\ WDARQSIIRKCGGPLRRGAPGLLKG DGEGPKRKS
1886	7383	A	2023	3	634	
1887	7384	A	2024	131	546	VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLSFHLEMIHPR CESWKMPGALPM/YCSP/CCLLVLL KDQGGGASTGVRRRKESWLPAPHS STVQVTQEGWREQSRELPKTECQL GWFLFLLQPYSRSFY
1888	7385	A	2025	363	578	RPYPCLSPRSSSTNPLSS**LNKIPS

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						LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK
1889	7386	A	2026	166	191	KNVIHQSKNCVFKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYPPARQPAPADHRQWPVPQ RGPEASG
1890	7387	C	2027	358	405	MSSREGARDGGEGLRS*
1891	7388	C	2028	306	347	MSPGRGPGMEGRG*
1892	7389	A	2029	2	358	QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRHLQASSCPPAHPLP PTQSCSSCQGWLCPPQGCPPGGPRT A/CIVPWPSFVASAATQERGQCPL DPLSPNQTRALHLSGTSGK
1893	7390	B	2030	1043	1146	MPSSVSWGILLLAGLCLVPVSLAE DPQGDAQAQKTDTSHTDQDHTFNK ITPNLAFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACLTSSHX *
1894	7391	A	2031	2	402	SQTQREPTMVLSPADKTNVAAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNVAHVDDMPN ALSALSDLHAHKLVRDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLTSKYR
1895	7392	A	2032	9	509	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAGHAGEYGAEALERM FLSFPTTKTYFPHFDL\SHGF\AQVK GATAKKVA\DALTKAVA\HVDGHA QTALSALSGPATAHKL\RVGPGSTF KLL\SHLPCWLT\GRPPSPAEFQPLA VARLPWNKVPGLLVEAPLLEPSK
1896	7393	A	2035	413	674	CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGSQRPPPGP\SD SPASASRAWPQTAH
1897	7394	A	2036	2525	2734	LTNGTESTPPPRPTPSRCSRQRCPE VGPPF\CSPFFCVPAHFKLLPWTFQG TVISSPQIISSSSVCAFF
1898	7395	A	2037	168	392	NKSFFPPSSSFDLSILNTFSFPLTLSSL RSGPTHHTHTHAN/THHTHTHTHT HTPSSDPQAHPHTLTDNWVSTL
1899	7396	A	2038	216	528	AGEKLGLGAGDTSWRVWVPAACT PGRVERVGWCRV\GPADPSGGLTPG \ACGASWQGPFSWAKDLQGPWSW WPVWPTRPFLDLGSSGLLIWVHK WPWGVCVYV
1900	7397	A	2039	37	424	RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPFAP*PQTGC WSPDGSRLFTVLGEPLIYSLSPER CGEGKGVALEVQSQRLLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL

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1901	7398	A	2040	1	442	PEFRVDDFVLRYPAYESSPGTELRECGL/WPFRPGVCRLQTSCEPWINLPVLQLTKDPLKTPGRLDHGTRTAFIH HREQVWKRCINIWRDVGFLGVLNEIANSEKEVFEWVKTAGSWALALCR WASSLHGS�FPHLSLRNEDLIAEF
1902	7399	A	2041	722	1395	CLCLGLWACQS\CILIWTLDPSTSLF\TRPSSG\CAQVLSHPGHPTVTS LAW APSGGRLLSASPVDAAIRVWDVSTE TCVPLPWFRGGGVNTLLWSPDGSKI LATTPSAVFRVWEAQMWDLWRRW PTLSGRCQTGCWSPDGSRLFTVLG EPLIYSLSPERCGEKG\ALEVQSQ QRLW\QICLRQQ/YTRHQMVRRLG ERLTPWSGTPVGNVWLCFMKGKA QGLPGW
1903	7400	A	2042	1	418	MPEQEPTAEQLS*IAAENEDEHSV NYKPRAQKSIQEIQELDKDDESLRK YKRALLGRVAVSADPNVPNVVAP GRVLLPQALSATTPGRPSLTQPGT NKGPSAHIAESRLCLPRPIPLRVV SARLRQRRLSLLLF
1904	7401	A	2043	1	525	LSQQASLESF*KHFFCLKEVVEYRIK ISFRVNREIVSGMKYIQHTYRKGVK ID\KTDYIVGSYWPRAEYEFLTPKS PRWTASPTPSVLQSGAPLGHQYLLP PSVPSSGHWPGVCSPRLLVPPLLGR PSLTLPGTNKGPSAHIAESRLCLPR PIPLRVVSARLRQRRLSLLLF
1905	7402	A	2044	354	487	
1906	7403	B	2045	61	516	KSIQEIQELDKDDESLRKYKEALLG RVAVSADPNVPNVVVTGLTLVCSS APGPLELDLTGDLESFKKQSFVLKE GVEYRIKISFRVNREIVSGMKYIQHT YRKGVKIDKTDYMGVSYGPRAEY EFLPRPIPLRVVSARLRQRRLSLLLF*
1907	7404	A	2046	11	328	
1908	7405	A	2047	1	507	LTFVCSFRPVPLYDLRSNLD SKNQ SFLFKEAVDYRIKISFRFHPKYISLI*\ YIQHTYSK/GVKIDKTDYMLGSY/GP RAEYEFLTPVEEAPKGMLARGSYS IKSRFTDDDKTDHLSWEWNLTISIY CLRPCRPWATGLAPVPPGSQCHHPR QAFDPARNKQGTKCTHC
1909	7406	A	2048	1	327	TAEQLAQIAAENEDEHSVNYK/PP AQKSIQEIQELDKDDESLRKYKEAL LAPLAVSADPNVPNVVVTGLTLVC SS/APGPLELDLTGDLESFKKQSFVL KEGVECTVGPH
1910	7407	A	2049	1	452	
1911	7408	A	2050	3	868	SHFVLDPVPGVGHLLTPQRMPLSRN RGGGEERRCPPWSPFGAPLQPTLLL RSAPPLGIQVQGLSPSRPQVSRPLS LSMAEQEPTAEQLAQIAAENEDEH SVNYKPPAQKSIQEIQELDKDDESL RKYKEALLGRWPFSADPNVPNVV

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						VTGLTLVCS\SAPGPLELDLTGDLAE SFKKQFVLCLKEGVEYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMGVSYG\PRAEGSFELTPVEEAP\ KGMLA\RGSYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD
1912	7409	A	2051	1	618	TLLVPQDSERTHPWLLSPADK\TNV KGPPGGKVGAAHVRSMCAEALER MFLSFPTTKTYFPHFDSLHG\SAQV\ KGHG\KKVADALTNVAHV\DDMP NALSA\SDLHAHKLRVDPV\NF\KL LKPLACLVDPGPAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFELQIPV KLGSLGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS
1913	7410	A	2052	3	398	
1914	7411	A	2053	1773	3913	FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLLE MVKLTSMRGQFLEAQIPTGISLTLQ YQLYQKQTNKNMSYSFVFLKWV ALGQRRAGYPSLEDADSRFNGS RSFLITVIGITLVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRRAVEAQPKDRTWDVGKG QGTEGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLLLAGLCCLPSSLVED PQEDAAQKTDTSHTDQGDWEDLA CQKISYNVTDLAFDLYK\SWLIYHN Q\HVLVTPTSVAMAFAMLSLGTAKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRLPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKEQINNYVEKRTGRKVV DLVKHLKDTSLALVDYISFHGKW KDKFKAERIMVEGFHVDDKTJIRVP MINHLGRFDIHRDRELSSWVLAQH YVGNATAFFILPDPKMMWQLEEKL TYSHLENIQRAFDIRSINLHFPKLSIS GTYKLKRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVLTIDEK GTEATGAPHLEEKAWSKYQTMFN RPFLVIIKEYITNFPLFIGKVVNPTQK
1915	7412	A	2054	3	409	PGPVVVSNNSSAHGSQRTSGPESSM K\YCCPEMVEYQKKGKSLDSEPSVP SAAKPPSPEKTAPVASTPSSTIPALS PPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLY
1916	7413	C	2055	235	366	MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG*
1917	7414	A	2056	3	484	STTPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWVVE NR*LSLGHR\APSFPSPPA VSASFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG

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						PESSMKGTIT*KTLSSQSFKNINKVF VVSELYTQK
1918	7415	A	2057	2	4256	FVHGSMADTDLFMECEEELEPWO KISDVIEDSVVEDYNSVDKTTTVSV SQQPVSAPVPIAAHASVAGHLSTST TVSSSGAQNSDSTKKTLVTLIANN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQANHVVTSSP ASQPIFITTQGFVVRNVRPVQNAMN QVGIVLNVQQGQTVRPITLVPAPGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTTNTFTTVIPATLTIRSTVPQ SQSQQTKSTPSTSTTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSPSP AVSIASFVTVKRPGVTGENSNEVAK LVNTLNTIPSLGQSPGPVVVSNSS AHGSRQTSGPSSMKVTSSIPVFDL QDGGKICPRCNAQFVRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSSTPIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHMKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHMKDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNGNAFQQHYM RHQKRN VYHCNKCRLQFLFAKDKI EHKLQHHKTFRKPKQLEGLKPGTK VTIRASRGQPRTPVPVSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYALFKNSVSGI KLACTSCTFVTSVGDAMAKHLVFN PSHRSSSILPRGLTWIAHSRHGQTRD RVHDRNVKNMYPSPSPTNKAATV KSAGATPAEPEELLTPLAPALPSPAS TATPPPTPTHPQALALPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKKLRVVLFAALCC NTEQAAEHFRNPQRRIRRWLRRFQ ASQGENLEGKYLSEFAEEKLAEWV LTQREQLPVNEETLFQKATKIGRS LEGGFKISYEWA VRFMLRHHLTPH ARRAVAHTLAPKDVAENAGLFIDFV QRQIHNDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSILLEAKESGYSDDEIME LWSTRVWQKHTACQRSKGMLVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQLDVCIKRTVKNFLHKK WKEQAREMADTACDSVLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPGPDGNINSPTRNADMQKELIA SLEEQLKLSGEHFESSTPRPRSSPEE

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						TIEPESLHQLFEGESENE\SFYGFEEA DLDLMEI
1919	7416	A	2058	3	824	
1920	7417	A	2059	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\SCMAALTVTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVPYAKTQPLQHNNLLVCSVNGF YPGSIEVRWFRNGQEEKTGTVVSTGL IQNGDWTFTQLVMLETVPRSGEVY TCQVEHPSLTSPSTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS
1921	7418	A	2060	2	867	GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLTVTLMVLSSPLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQEEENVRFDSVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVPYASRTQPLQHNNLLVCSVSGF YPGSIEVRWFRNGQEEKTGTVVSTG LIHNGDWTFTHTLVMLETVPRSGEV YTC\QVEAPRA*QAPLTVE\WRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPRGFLS
1922	7419	A	2061	3	940	RNFRVDPRVRREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RT\VSLMV\SSPLALAGDTRPRLW QPKRECHFFNGTERVRFDRYFYN QEEVRFDSVGEYRAVTELGRPDA AEY\WNSQKDLLE\QRRAA\VDTYC RHNYGVGESFPVQRR\VEPKVTY PSKTQPLQHNNLL/VFCVSGFYPGS IEVRWFLNGQEEKAGV\VPQALIQN GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLLPLGPGLFIY FRNQKGHSGLQPTGFPELCKR
1923	7420	A	2062	25	384	EFHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAVVRSMCAEALERMFL SFPT\TKTYFPHFDL\SHG\SAQVKGP RQRRWPNALTKRRGAPLDDMP\NT ALSALSDLHAHKLVRDPVQLSSS
1924	7421	A	2065	47	353	AGRVRLWDCVEVDLTGAGQSV EASRHAWEVVRNRCHWAPQLFLS FAPGWGG\GEGRVGDGGA\VGWFPS PQPPSSPPGVMPCPHRRGTEPGRD LVPAQ
1925	7422	A	2066	3	692	KRLPKMAEVQVLVL\DGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVV\RCE G\NISGNFYRNEVKVPWLFPSKR\M NTNPSRRPLTTSGAPSRIFWRTVRG MLP\HKTQAEAKAA\LDRL\KVFDGI

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						P\PPYGQEKSGMVVPAALKVVRRLK PTRKFCLIFFFSGGGAL\AHQ\VGWK YQAVTAP\LEE\KRKREKPRFHYRK KENSIMRL\RKQAREETWRKKIDKY TEVLKTHGLLV
1926	7423	A	2067	1	2091	
1927	7424	A	2068	384	4189	ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETEVEKGGKRRGRPRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFQICSGCRGTVRIEMFRNM QNAEIIRKMTTEFDEDSGDYPLTMP GPQWKKFRSNFCEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLMTALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRY\RDAAIEIRAICIE\IGV WMKMYSDAFLNDSYLKYVGWTLH DRQGEVRLKCLKALQSLYTNRELP KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEALSNEDECENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEALAKRRGRNSPNGNLI RMLVLFLESELHEHAAYLVDSLW ESSQELLKDWECEMTELLLEEPVQGE EAMSDRQESALIELMVCTIRQAAEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADA EK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVES\DVLEACS KTYSILCSEETYIQNRVDIARSQID EFVDRFNHNSVEDLLQEGEEADDDDI YNVLSTLKRITSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQQCLSNVNT VKEQAFMLLCDLLMIFSHQLMTGG REGLQPLVFNPDGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLIYDIVDMHA AADIFKHMYKYYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNELVQ EQGPNLDRTSAHVSGIKELARRFAL TFGLDQIKTREAVATLHKDGIEFAF KYQNQKGQEYPPPNLAFLEVLSEFS SKLLRQDKKTVHSYLEKFLTEQMM ERREDVWLPLISYRNSLVTTGGEDDR MSVNSGSSSKTSSVRNKKGRPPLH KKRVEDESLDNTWLNRTDTMIQTP GP\LPAPQLTYTVLRENSRPMGDQI QEPSEHGSEPYFLHNPQMQISWLG HPKLEHLNPKDITGMNYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDMN\EEF\EDTM\VIDLPP\SRN RRERAELRP\DFVDSAAIIEDDSGFG MPMF

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1928	7425	A	2069	1	2661	
1929	7426	A	2070	1	1454	
1930	7427	A	2071	1	2364	
1931	7428	A	2072	1	1368	
1932	7429	A	2073	114	1473	VKGDRFGALRFNDPCAGIKLPMTFF TELEKTTLKFIWNQKRARIAKSILSQ KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTGPSEITPHT YNYLIFDKPEKNKQWGNDSL FNKW CWENWLAICRKLKLD PFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLKS FCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPAIPL LGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVG TWMKLEIHL SKLLQEQKTK
1933	7430	B	2074	1	1890	MDKFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFTAEF YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASIIIPKPGRDTTKIENFRPIS LMNIDAKILNKILANRIQQHIKKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMII SIDA EKA FDKIQQH FMLKTLNKL GIDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVMELLARAI RQEKEIKGI QLGKEEVKLSLFADDMIRIKYLG IQ LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTEPSEITPHIYNYLIFDKPD KNKQWGKDSL FNKWCWENWLAIC RKLKLPFLTPYTTINSRWIKDLNV RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLKS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHPSEKCKSKHNEIPSHTS*
1934	7431	A	2075	1	2676	MKAEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHNRKQERPKI DTLTSQLEKEKQEQT HSKASRRQE MTKIRAE LKEIEIQKTLQKINESRSW FFERINKIDRPLARLIKKKREKNQID AIKNDKGDITDPTEIQT TIREYYKH LYANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPI TGPEIVAIINSLPTK RSPGPDGFTA EFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASIIIPKPG

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						RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQG WFNIRKSINVVQHINRTKHKNHMI SIDA EKAFDKIQPFMLKTLNKLSD GTYLKIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTAWYWYQKRDIQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKTLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLKSFTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIKKSGNNRC WRGCGEIGTLLHCWWDCKLVQPL WKTWVQFLRDLELEIPFYPAIPLGI YPKDY
1935	7432	A	2076	1	3045	MDKFLNTYTLPRLLKQEEVESLNRPI TGSIDIEAINSPLTKKSPGPDGFTAE FCQRYKEE/LEKEGILPNSFYEASHIL PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIPG MHGLFNICKSVNIIQHINRTNDKNH MIISIDA EKPFDKIQHFMLKTLNKL AQNLLKLIGNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCSWEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLKSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSCSF SRCTVQAAGGSAILEDGDPLLTAPL GSTPQAAVCRGPRGRELRAAPADS

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						HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCFS PSDPQNLQKGEGCPSLVRASAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLEYEQA
1936	7433	A	2077	1	2142	
1937	7434	A	2078	1	1551	MRFKEKIHLHNIKEPSEAASADGGA VASYPDLAKIVDEGRYKAEVMQLR CGWRAPASDCVHSAVVGVDVSL EVLARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPTVSAQNLLKLIS NFSRVSGYKINVQKSQAFLYTNNK QTESQIMSELPFTIASKTIKYLGIQLT RDVKDLFKENYKPLLNIKEDTNK WKNIPCSWIGRINIVKMAILPKVIYR FNAIHIKLPMTFFTELEKTTLKFIWN QKGVHIAKSILSKKNKAGGIMLPFH KLYYKATVTKTAWYQYQNRDIDQ CNRTEPSEIIPHIYNHLMFDKPDKNK KWGKDSLFSKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPK PIKTLEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKLKSFTAK ETTIGVNRQPTTELEKIFAIYSSDKGLI SRIYKELKQIYKKKNPIKKWVKD MNRHFSKEDIYAVNRHMKKCSSSL VIREMQIKTTMRYYLTPV
1938	7435	A	2079	1	1458	GLSGDLLGAHQLPDVLGCVQPLPD LLLPPQNLLALQSLQDDLLWALDP AAAAPWAMDRGAATQWAVGPVV SDPWVMEAVASLPSAMDLDAAQ TWLLGAASLLVTDQPMQPSADQL AEFPDLLSKVSQSLRIKYLGIKLTRN VKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFN APIKLPMTFFTELENTTLKFIWNQK RACIAKSILSQKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWN GTEPSEIMSHIYNLYLFDKPEKNKQR GKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIHT LEENLVNTIQDIGMGKDFMSKTPKA MATKAKIDKWDLIKQKSFTAKET TIRVNRQPTTEWEKIFAIYSSDKGLIS RIYKELQQIYRKKTNNPIKKWAKD MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPV
1939	7436	A	2080	1	2028	
1940	7437	A	2081	2	1547	
1941	7438	A	2082	3	1945	
1942	7439	A	2083	1	2124	
1943	7440	A	2084	1	2250	
1944	7441	A	2085	2	2483	GKYYKLSSGTAPTCVSLGWGLARG

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						DSAAPALGSRTSACAPCSHGTTWKL SLEPSDRLSPCDRSSEEATHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKAGGPVI CRSLPESRGFLWASEGRKCMLIGSW AAMGRLRKSTISSRFQPOTLAGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPQTHWEFELS EDYNKMTPVKNYQVLEVLARAMR QEKQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRGVDQWNRIEPISEH PHIHNHLIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLDPFLTPYT KINSTWIKDLNVRPKTIKLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLPRIYKELK QIYKKKSNNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIIKSGNNRDM DEAGNHHSEQTIARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPIVG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIYI QPAPKS
1945	7442	A	2086	1	2622	
1946	7443	A	2087	853	2831	YPESTMNSNKFTRKKQTTSPKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRSK SQDRKD*QSTLLAILIKKKGOKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDTYTLPT LKQKKEVKTLNRPITGSEIEAIINSLP T/KKSPGPDRFTAIFY/R/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR* HHCIFRKP HHLSPKSS*ADKQLQQS LRJQNQSAKITSIPHQ*QTNREP NHE *TPIHNCFKENKMPRNP TYKGCESG LQELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDFFRIGKNYFKVHMEPK KSPHRQVNP KPKEQSWRHHTT*LQ TILQGYSNQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLQRT*TNLQDKNKQPHQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VGKGYEQTLKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN
1947	7444	A	2088	1	4954	MVFSIDAQKAFDKIQHRFMLKTLN KLGIDGTYLKIIRAIYNKPTGNILNG QKLEAFPLKTGTRQGCPLSPLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLKFENYKPLLNEIKEDTDK WKNIPCSWIGRIHVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIKSIKLSQKNKGGGITPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSNNSEGLNPGYKGFPTIHWAPL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGVFISSASQAF TKKARIYARLRVSQALKTLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFLLEL NQKSQQYQKQEQTHSKASRMQEIT KIRAEKIEITRKTQKIDESRSWFF ERINKTDRPLARLTQKREKNQIDA IKNGKGDITDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVDSLNRPTGAEIVAINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKGR DTTKENLRPISLMNIDAKILSKILA NRIQQHIKKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFMLKTLNKLIGIDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNNDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFK\ENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEKTTLKFIW NQKRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHS LFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK

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						SFCTGKETITRVNRQPTWEKIFAIY SSDKELISRIYKELKQIYKKK\TNNPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMAI\IKKSGNNRCWRGCGEVGTLL HCWWDCNLVQPLWKS\VRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTMEYYAAIKND EFMSFVGTWMKLEIILSKLSQEQT KHRIFSLIGGN
1948	7445	A	2089	93	225	
1949	7446	A	2090	133	849	PVWPKWSGWPLLMRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STPDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVLPLARIAT VVIGGVVAMAAVPMVLSAMGFTS VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTPDPKATELTRAGMEASALTSSA VTSVAKVVRVASGS\AVVPLAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRSCGPMAGC ANGCSSAMGLQLRAGIALVLP
1950	7447	A	2091	161	1344	TCPVLRHYHSTMSSHKGS\AVAQNG APASNREADTVELAE\GPLLEEKGK \RVIANPPK\AEEEQTCPVPQ\EEEE VRVL\TLPLQAH\HAMEKMEEFVYK VWEGRW\RVIPYD\VLPL\W\KGND\ YLLHGH\RPMP\SF\ACFKSIFR\I\TE T\GNI\W\THLA\L\GFV\LF\LGILTML RPNMY\FMAPLQ\EKKV\VF\GMFFLG AVLCLSFS\WLFHTAY\CHF\GGV\FSTF PQREL\FKGLLL\LN\MGELWSPGLYY SFYCSP\Q\PRLIYLSIVCVLG\ISAIV AQWDRFATPKH\RQTRAGVFLG\LG LSG\VVPTMHFTNRWRALSKATTV GQ\MGWFFLMAV\MYITGKLAFNAA \RIPERFFPGK\FDIWFQSHQ\IFHVL\ VV\AAAFVHFYGS/VSNLQEFLTGL EGGL
1951	7448	A	2092	2	1419	RLRDPYRSSRLCRRGASRTSSAARS RSRSPA\VEGCN\RS\PGAPQAPARR RPSRGAPGRAMVKVA\FNSALAQK EAKKDEPKSGEEALIIPDAVAVDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIK\DDVILN/ESPSADAP AA\LYQTIE\ENIK\IFEERRSLNFISVP VPEF\ADSDPAKIVQDFN\RKLTA\YL DFNL\DKCYVIP\LNTSMCYATPKTL LELLINIKAGNLFALSPYLD\SMRHM GYLLDR\ENIDHLGF\FIYRLCHDK\ ETYKLATRRLKLFKGIQ\KREGQQLF SAISGIFENKFAVET\LICSW

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1952	7449	A	2093	1	669	
1953	7450	A	2094	267	550	GRTMMFGAKRRQEEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQELRGTVSNCKNM\VRG\LDEDET TFLDEVSRQQELIEKQPKRRRT
1954	7451	A	2095	1	418	
1955	7452	A	2096	272	383	
1956	7453	A	2097	118	379	RSGGGRGRRGPEVLHLKHPMLKRP DFLYRKPFSSRGWEHGPPSRKSHLL/ GAPPPFPKFFCHLC*APSPFRVLSPY QKRIHLVPPTQLH
1957	7454	A	2098	1	276	
1958	7455	A	2099	1	341	
1959	7456	A	2100	1	450	ACPYLALNSSMFCPDLILPTCLISST GFVGEKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLPCHAHYHSRCVDPWLTQ TRKTCPIK\QPVHRGPGDEDQEE\ ETQGQEEGYEGE\PRDQP\ASERTPF LG
1960	7457	A	2101	238	525	
1961	7458	B	2102	178	373	XLPQPLRGPLAHSDDPERPAPFASSLF IGVLGKTKRKLKKGKEEGDERGS KGTNPALRKDPTFGF*
1962	7459	A	2103	634	1940	SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQPLSSRCHAPLQPFPLPV VVA AVLWGS GPD PGASFRATS DH NCQH GIFA DLPALF GATLSLEG PQG L\LGE PHPDNACSPIAPPPAPVNGS VFIALLRFD CNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGERSSEYLRLAFVYE KGARVLLVPDNTFPLGYLIPFTGIV GLLVLAMGAVMIARCIQHR\KRLQ RNRLTK\EQLNQIPTQTNQKRDQY DVCAICLIEYEDGDK\LR\VFPGAHA YH\NRCVDPWLTQTR\KT\CPICK\Q PVHR\GPGDEDQ\EEETQGQK\EGDE GE\PR\DH PASERTPLL\SSPTLPTS\ FGFLRPKFPLVFS LGP\STD PPLSPPS SPCYPGLITPHTYTFG
1963	7460	A	2104	25	527	EFHRLRENPPMVA VSCPTKTNVKA\ AWG\KVGAH A VRSMCAEALERMF LSFPT\TKTYFPHFDL\SHG\SAQVKG ATGKKVADALTNAV ANVDDMPN VAVRPEATLHAHKL RVDPV\NFKL LKPLACLVDPGPAHLRPSFTPGGA TSSLGQSFLGFLK HRCNLNPNYR
1964	7461	A	2105	262	364	
1965	7462	A	2106	3	1265	PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLDGD KARPRAQLRRESG GAESVTRPLRAAS PAPPRAARA MSEKPKLGRAP SASLSARCRAPR CCSCRARRPRIP PQCPRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSST

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						AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPQCAPTPTHRAP CAPTASIASPGVRPPLPIAPPGVRPR LPITPPMEGVKTENDHINLKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRF\RFDGQPNQWKLLDDL STAGDWKDEDTIDVFSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCGNSRTFTT MIFLSLMYFKLQLKTISAGMNL
1966	7463	A	2107	4	408	
1967	7464	A	2108	1	465	PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCFLGLGPAI*SPHPQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQ TANQCILPQASSTLCC*LHPQ NLVCP
1968	7465	A	2109	126	488	
1969	7466	A	2110	1	5586	
1970	7467	A	2111	68	310	TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETQHRELDKTRARGPE*GS VVLTSPLWSPCRKCATGTYHGSPH CQSSGGGR
1971	7468	A	2112	2	630	FFFFSDDLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSSFSRISFSVSGICPWWSR DGEVGTTFPSQFAKGRKGLIRRGPP QHPLRLSPGPIEEQK*GLVSPKARLG ISPCQLCPGFWSYLDSPSPPGGSC SGCTVPGSSHNVSVPVSHPSGPACGV RTALSSA
1972	7469	A	2113	331	754	NFLKTNNVWSKWTHVLSQFWYQG FJLFCLGSIVKCTEIDSSICTE\PSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQKDNMGEMNGTT TTKTFCFIFMPGEDQGCSSCVSTRTT RKSQVQKSRGTISRIFYHK
1973	7470	B	2114	110	225	XLGRPQLAGSLRSRFPISGMRGEFFT QDCQRNAGREELQGRLSIQSFSPILA LGPDDSCETKTGMDKLS*
1974	7471	A	2115	83	287	SLLKCSGVIVLRRPLGYGQVMK* PGAAY*GRTG*SHPPFSTDWSTDTG VRKSIWCHRNCRWESPS
1975	7472	A	2116	167	397	EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWGDEGHWP TPNRS CLL
1976	7473	A	2117	1	540	FCHLQIYYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRRKLLNLSLGLSLLKFLGSVPGGT AGMGKSVPLSPSQVCCGFRSFNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWVTYPALSLSFNKSQCPWVFP LPTMPPG

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1977	7474	A	2118	1	3121	RQEAE LARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYLVT IAKACALDPGTRATGGSLSSTGNDT SEACDADFSSLTACSGVESTAAPQ KLLILDARSYTA AVANRAKGGGCE CEEYYPNCEVVFMGMANIHAI RNSF QYLRAVCSQMPDPSNWL SALESTK WLQHL SVM LKAAVL VANTVDREG RPVLVHCSDGWDRT PQIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLANNPCEREKRN YKRTCSVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTAVYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDL SACS DTS SPLTRTSSDPNLNNHCQEV RVGLEP WHSNPEGSETSFVDSGVGGPQQTV GEVGLPPPLPSSQKDYL SNKPFKSH KSCSPSYKLLNTAVPREMKSN TSDP EIKVLEETKGPAPDPSAQDELGR TL DGIGEPPEHCPETEAVSALS KVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTPLDPSTDFLNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLLENPRFGKMPLELVRKPISQSQI SEFSFLGSNWDSFQGMVTSFSPSGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSSHSNGH CTGPGGKNQMWLSSH PKQVSSTKP VPLNCPSPVPPLYLDD DGLPFTDVI QHRLRQIEAGYKQEV EQLRRQVRE FQ\MRLDIRHWCAPPAEPPMDYEDD FTCLKESDGS DTEDFGSDHSEDCLS EASWEPVDKKETE VTRWVPDHMA SH\CYNCDCEFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS
1978	7475	A	2123	3	259	FPHRAGPILSSFQVPQRWL VGGFGR NCIAGGESV VWDRTN KYTRN* AQE WGMFWSLDGHLGESIIRGRSNTG ALSCPWPLGHL P
1979	7476	A	2124	1171	1784	KLYSLSVLYKG EAKV VLLKPA\YDV SSFSFF\QRPTVQE\FMTFTS QLIVER S/SRKGTRASVKEQDYLCHVYVRN DSL AG/VVVIADNEYPSRGGPFTLL\ EKVLDEFSQAKSHRIDWPVGIPWL TIHYPALDGHL SRYQNPRE\ADPMT KVQAE LDETKIILHNTPWESLLERG EKLD DLVSKSEVLGTQSKAFYKTA RKQNSCCAIM
1980	7477	A	2125	2	262	RGNWVFLHTTEFSLTRSLISFN SCFI TRLECSGAITAHCSLDLLGSS/QSPTS

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						PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV
1981	7478	A	2126	36	376	PFDPAVLTAKA AVRALVASRLAAA SAFTSLSPGGRTSPSQAALHLSVPRP AARVALILVHLSRGGAEVQIFAPD VPQMHVIDHTKGQPSGESRCGGGI GTCFLSTSHGAAFF
1982	7479	A	2127	3	724	LAAASAFTPLCPVCRTSPSQAALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGAEVQIFAPDVPH MHVNDHTKGQPSGESMNVLTES ERIRRGKITDLANLSAANHDAIFP GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSKDLPGH CPGRPLKWSLRKRCRLRAPEGGCP CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREPMALSSVTD
1983	7480	A	2128	172	1020	PSDPAVLTA MA AVRALVASRLAAA SAFTSLSPGGRTSPSQAALHLSVPRP AARVALVLSGCGVYDGTIEHESA\ ILEHLSRGRAEDHIFAPDVPHMHVI DHTKGQPSGESRNVLTESARIARG KITDLANLSAANHDAIAIFP/GEGFG AAKNLSTFCRWTGKICKVNKEVER VLKEFHQAGKPIGLCCIAPVLA AK VLKGVEVTVGHEQEEGGWPYAG TAEAILALGAKHCVK\EVVEAH\VD QKNKVVTTPAF\MCETALHYIHDGI GAMVRKVLELTGK
1984	7481	A	2129	1	416	IQYRSDELHSITMKKGGVFLFGII LLVLIAAHGTPVVRKGRCSII TNQ GTIHLQSLKDLKPFGPSQCKIDIIA TLKNGIQTCLNPSAD\VKELIKKW EKQVSQKKKQKNGKKHKQKKV LK VRKSQRSRQKKT
1985	7482	A	2130	2	81	
1986	7483	A	2131	2	130	
1987	7484	A	2132	1	524	RPRIRHEPQTQREPTMVLSPA\DKTK AQRPPRLKLGATPGEYGGEP LER\M VLFPPPTPKPYFPHF\DL SHG\SAQVK GATAKKVA\DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHLPCLGEPWAGPPSPA EFHP LAVARLPWQSFLLGFLKHRCLNL PNYR
1988	7485	A	2133	388	654	GLFFVLQFFFLFCFVFLRSHSVSQAG VHWC RHGSAAST/SPGSSDPPTLAS\ KVLGVTDM SHCTWAESYFFTKMGS SPVVACACSSSYLGG
1989	7486	A	2134	384	622	INAPPRCPQLCTSEVCAME/CPQ RV PAGPCPGCPRGNLLIHAPSNRP GTTS QINDPQPFLRICFWGSPKTPSHRHKS FFF
1990	7487	C	2135	44	340	MKCSQPXRCHFQSDFOKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGVVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV

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						P*
1991	7488	C	2136	2413	2829	MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCALLPSPEPTGSVNVI FYVPLPSGLLSTSAPGSRASGVGVL LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGDQEALVQGALGW GQRAWTPAQCSVDNG*
1992	7489	A	2137	69	332	YQVLKTDKNMSRISFFFLRKGLAL SPRMECSGAITAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS
1993	7490	B	2144	73	358	XVPGSRGPETKLWDDFSMSQATKR KHVVKEVLGEHIVPSDQQQIVRVLR TPGNNLHEVETAQQQRFLVSMPSK YRKNIWIKRGDFLIVDPIEEGEK*
1994	7491	A	2145	80	201	
1995	7492	A	2146	498	748	FLPRRGDNDSPQ/WTKACCRRRRT CW*T*TWWIRSGQRKMWSCGRRSL TTCMPRTRTAARLMACGSGSWRR SGPSCGCRLSP
1996	7493	A	2147	1	1764	MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLKDTCGANAK QSRDCFGCLRE/WCAKSRPAAEVSE LKADSKEGPQAQGPEQERTGL
1997	7494	A	2148	842	1186	FLPRRGDNDSPQ/WTKACCRRRRT CW*T*TWWIRSGQRKMWSCGRRSL TTCMPRTRA WTTWRSKNLALSCP SMTKSLKGSGHIPSAWSRAARLMA CGSGSWRRSGPSCGCRLSP
1998	7495	A	2149	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMKTSFREWLK DTCGANAK\QSRDCFRMPFEKWCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD\CYC\RTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWPVSWVTVYQLFLEWDFP GPIPHPHPHFQSV
1999	7496	A	2150	150	446	HEGLLLKLRLSDVYFLLFFETRSCF VAHAGVQWHHYNLSL/T/PPGTPMF PPLLASQVAGSTGMNHQAQIIKKT FGENMILLCCSGWLSGIFVLYSLY
2000	7497	C	2151	203	427	MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQQAD LLNGQCGFQQSSEPQPHVHTTSS*
2001	7498	A	2152	1	1065	
2002	7499	A	2153	597	1292	QTFSNTIFLLTRHKQHSMILVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVR\VPATNLILGEGRGFEISQG RLGPG\RIHHCMRTVG\WAERLLQI MCERATQRIAFKKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMIDL GSAGAKKEIAMIKVAAPRAVSKIVD WAIQVCGGAGVSQDYPLANMYAI TRVLRADGPDEVHLSAIATMELRD QAKRLTAKI

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2003	7500	A	2154	1694	1886	ASDSRVPA PGIS/PSAPFPTQLSPRRS PPSPPPPPQSP LGIFSPKASPVGILHL FKTLFCILNV
2004	7501	A	2155	1002	1480	MLLLKTTERFEVSVCMACTYV\SNL GKKQRSVSFLASGLMRVSTGPELRL HHSFVLTGDVGRRICRLLVGLFTKG DTSSKR V\HPFSPGP\CFLLCDLAR V GSSPKINRVPHFTRTQTSTQRSCTVF VWQRCSLVGPFQVT VFTMYFHHS RSISRFS SG
2005	7502	A	2156	1	1623	RLPFVDVDARVYADAPAKLLLPPL AFWELAVRLRGAEAA SERQVYSVA VKLLLLHPAFQSCLLLTLLGLWRTT PEAHASSLGAPISAASFLQDLIHRY GEGDSLTLQQLKALLNHLDVGVGR GNVTQHVQGHRNLSTCFSSGDLFT AHNF\SEQLRIGSSELHEFCPTILQQL DSRACTSENQENEENEQTEEGRPSA VEVWGYGLLCVTVISLCSLLGASV VPMKKTLYKRLLLYFRALAIGTLL LKRLFQLIPGAVWFQPLEDYYVSKS AVVFGGFYLF FTEKILKILLKQKNE HHHGSHYASESLPSKKDQEEGVM EKLQNGDLDMIPQHCSSELDGKA PMVDEKVIVGSLSVQDLQASQSAC YWLKGVRYSDIGTLAWMITL\SDGL HNFIDGLAIGASFTVSVFQGISTSVAI LCEEFPHEL GDFVIL\LNAGMSIQQA LFFNFLSACCCYLGLAFGILAGSHFS ANWIFALAGGMFLYISLADMFP NEVCQEDERKGSILIPFIIQNLGLLTG FTIMVVLTMYSGQIQIG
2006	7503	A	2157	1	604	MGTRWEPGW RAPGLAPAAQARSS GRAAPAAGSERARERERDGGSVGG GGSSAIPSERAA DAHGEDSGAYR WERANRPFSNNCCCLAFYLGMEEA RWLYAGLFCVYGASLIAIATHVPLF GSQIKAE/DPSGDSAPAAHLPPQPAQ /PHLPQAQLMLTGSQLAGHPLGMR WSMATQHAGCVSQRCGLFPMTVG CSQGNILWSL
2007	7504	A	2158	22	1358	VHFSMGAPEIRMSKPLEAEKQGLDS PSEHTDTERNGPDTNHQNPQNKTSP FSVSPTGPSTKIKAE DPSGDSAPAAP LPPQPAQPHLPQAQLMLTGSQLAG DIQQLQLQLVLVPSHHLQPPAQF LLPQAQSQPGLLPTPNLFQLPQQT QGALLTSQPRAGLPTQPPKCLEPPS HPEEPSDLEEELEQFARTFKQRRIKLG FTQGDVGLAMGKLYGNDFSQTTF RFEALNLSFKNMCKLKPLLEKWLN DAETMSVDSSLPSPIQLSSPSLGF DG LPGRRRKKRTSIETNVRFALEKSFL ANQKPTSEEILLIAEQLHMEKEVIRV WFCNRRQKEKRINPCSAAPMLPSPG KPASYSPHMVTPQGGAGTLPLSQAS SSLSTTVTTYILSCGDAPPQPD SWR GWGRGRGCAPPQFHPLCHSPTPGH

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						HQQHKPQPLKAATRLSACQA
2008	7505	A	2159	3	452	
2009	7506	A	2160	9	633	NSARATDSERTHHGARLLPDKTNV KAAWGVGAHAGEYGAEALERMF LSFPTTKTYFPHFDL\SQRSAQVKG ATGKKVADALT\NAVA\HVD\DMPO TALSGPEATLHGAQSFQVDPVQLSS SLSHWPAWLTGPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFASPGQGP SLSWNPYPRWSFE
2010	7507	B	2161	55	372	MERFLMDGFQPPQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSPLPLYFVSAADGTNNVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN*
2011	7508	A	2162	552	1809	QLRGRGASRKWSALRRELGRRAWF ESQSPDWRQGPGRSVPLSSP HSEPHPEMAEDKTKPSELDOQKYD ADDNVKKICLGDSAVGKSKLMERFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHPFVPAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVTYRNLSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAILAVS YKQNSQDFMDEIFQELEVGVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMQGQASPATLFTNF SLEQEEEDVPDQEQSSSIETPSEEA
2012	7509	A	2163	807	1389	EPMAENKTKPSELDOQKYDADDNV KKICLGDSAVGQSKLMERFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSA\ADGTNNVKLFNDAILAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQSSSIETPSEEVASPHS
2013	7510	A	2164	3	923	RAARTRAEPEVECAAAARAGPAGVV RERAESRHGGRARGADPQRPWSLQ PSLGTARDNTLPSLGGPLSTARS QWAKNKTTPSELDOQKYDADDNV KKICLGDSAVGKFKLMERFLMDG\ FQPQQLSTYALTLYKHTATVDGRTI LVDFVHTAGQERFQSMHASYYHK AHA\CIMVFDVQRKVTYRNLSTWY TELSGSFRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAADGT NNVKLFNDAILAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQSS SIETPSEEAASPHS
2014	7511	A	2165	1	2715	
2015	7512	A	2166	1	2256	
2016	7513	A	2167	339	1086	IQMNRFL\LM\SLYLLGSVARGTSSQ

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						PNELSGSIDHQTSVQQLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSEH GSSKHTVAEHTSGEHAESEHASGEP AATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQKGKCLRGEGTCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLFSGHTRMQICCRNQSFCKNI
2017	7514	A	2168	2	425	
2018	7515	A	2169	2	169	GRVGDTLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVLDPYLGFQTHKMNT*FG S
2019	7516	A	2170	2	227	
2020	7517	A	2171	177	1400	LNAPGSQLSVGMKGLGESKNMVV NGRRNGGPLSNDHQNQSKLQHTG KDTLKAGKNAVERRSNRCNGNSG FEGQSS/RYPVSYGMTAKELCEND LATSLVLDPYLGFQTHKMNTSAFPS RSSRHF\SQSDSLSHNNPVRFRPIKG RQEELKEV\ERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLFE HVFIYLRMFATDSGFELPCNRYSE QNGAKIVATKEWKRNKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDCRPNCK FVSTGRDTACVKAL\RDIEPGEEISC YYGDGFFGENNEFCCECYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK
2021	7518	A	2172	3	114	
2022	7519	A	2173	328	471	
2023	7520	A	2174	1	190	
2024	7521	A	2175	2	132	SGLGRLPGPWQEAGSSRGPSSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIF/HAISPIPHF IAKRVTYDSATSSACRELAYFFT GIVVSCLWISPVILARVALIK\WGAC GLCV/VAGNAVIFLTIQGFPIFGRG DDFSWE\QWGYWTDfs
2025	7522	A	2176	191	479	NTSLPNPSEVSHSSLRLDSGGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM
2026	7523	A	2177	1920	2524	TQYPPAEQRSQTLMDQVFALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTIQTAFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQ PFVGGGTGVLKKPEGAGPAAPTS WRPRGEAPHRTGTAQPPTAV\SGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRCLKLDAGRRLRSGSKPHVK HL
2027	7524	A	2178	239	380	
2028	7525	A	2179	34	202	EPTTRQTLYMLITFTPHNHLVRETSS

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						VPFEQMKN*GSERFNTLSKALQTISAKTRI
2029	7526	A	2180	1	1566	
2030	7527	A	2181	574	1949	KSKCRFPEGLSEGFGPMRKEALSSG SVQAEAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIVQVAQAMSLTE DVLAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPKSHDVYWD IEGAVRRYVQPFLNALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNLLYVPELAHSPLYIQDKDGAP VATNAFHSPRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFLGIAQPHLPKCLLSGPTSEGL MTWELDRLLWARSVENLG\QATTT LTSLGAASWARSATLFIKGRRGHLE VLQRLAPVQKSAEELASGHLADLP LSPAREAVTSSELAFFDPSLLHLLYF PDDQKFAIYIPLFLPMAVPILLSLVKI FLETRKSWEKA
2031	7528	A	2182	76	419	
2032	7529	A	2183	71	350	AFIPAMAELIQKKLQGEVEKYQQQLQ KDLSKSMSGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETALQ LQQEFQRAQAAGAPGKA
2033	7530	A	2184	175	1032	GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHIHLTRIVGIGGTFDV SKLPFLSSPDLSKSMSGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFFP*PP FFSLPWISRFSTYLF\AFSTLHSESY* FLPFCLSPSLLSKRYESQLRDLERQ SEQQRETALQLQQEFQRAQAAGAPGKA
2034	7531	A	2185	112	520	AFIPAMAELIQKKLQGEVEKYQQQL QKDLSKSMSGRQKLEAQLTENNIV KEELALLDGSNV\VFKL\LG PVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETALQLQQEFQ RAQAAGAPGKA
2035	7532	A	2186	635	1015	GGQKHPTGLLKPPANTAATMPKRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKASAKKGEKL KGRKGGKADA\GKGLGNPNPAKNPR LPLHFQFQKAE\GTGGPLSEMFIFES SGTYW
2036	7533	A	2187	302	471	TLSHRVLVEAQSQREQLAALKKHHE EEI\VHHK\KEIERLQKRNL SRHK\QK DSKLLKH
2037	7534	A	2188	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGRV\WGVRTM\QA \RGFGSDQSENFPTGPRAPHP/RKAG

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						GALGKREQAEEERYFRAQSREQLA ALKKHHEEEI\VHHKKEIERLA FERHKQKI\KMLKH
2038	7535	A	2193	2	406	ARAEMSRVALAVLALLSLSGLEAI QRTPKIQVYSRHPAENGKSIFLKY VSG\FHPSDIE\VDLLKNGKE/RLKK VEPSDLS/FSAKDWSFYLLPYTEFH PQLKKDGVCPARVN\HVTLSAPRL VK\WDRRHVKQHQ
2039	7536	A	2197	319	393	WL/TPVIPTLWEAEVGGSFHRSSR
2040	7537	C	2198	84	290	MLPSKGLSFFSLQHLRDSRLLFPM SMITMLELECCRASSNEVRWLKX HXVSQICSLICFPXMLTIRA*
2041	7538	A	2199	2	743	PRVRSEVS\YRSLADPEPTGRD TMTYADLFKYIIIGDTGVGKTCFL LQFTDKRFQPVHDLSLGVEFGGSL CSTLME NQFKLHIWD\TAGQESFRSITRSY\Y RGAAG\ALLVYDITRALKPFNHLA S WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFARE\HGRIFR GTSAKTACN\VEEAFINTAKR\IYRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC
2042	7539	A	2202	20	222	
2043	7540	A	2203	1	458	RSSLTSLSNSAAMAPVKKPCGEG GAKKKKQVLKFTLDCTHPVEDGI MDAAQF*ASFCKERIKVKRKKLGT LSGGG/V*PIERSK\SKITVT\SEVPFS KRV/YLKYLTKKY\LKNNLR\DLV CRVVAYQPKRELRNYSYFQINQ\DE GREEDED
2044	7541	A	2204	2	321	FIFFSFSFFFFSFFSETGSCSVAQAG VQCHDHGSPQS/PNLPSSDLPTSAS KVLGITGVRHSLPPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS
2045	7542	C	2205	46	234	MTLRXWITWPFLFLSPSSKCLHLI ASILDLQLGSTHSSLSTIFFVVLAF RKIGLVCP*
2046	7543	A	2206	1	243	
2047	7544	A	2207	144	479	RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDS\LYAPGKAAVMTRKQS GYGGQ\TKPIFRKKAKT\KKIVLKA LSALSPTCRSKRMLAFKRWQAFNL LGGDKKRKGPSASS
2048	7545	A	2208	75	540	GGSGSVRVLRSSESPREEAVEEEVAA VAVVVAVAEAGTNQLRAETMANI AVQR\IKREFKEVLKSEETSKNQIKV DLVDENFTELRGEIAGPPDTPFERG RFP\LELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSV\TGAICLDIL\KDQWG SWQWT
2049	7546	A	2211	1	2640	MYSGNRSGGHGYWDGGGAAGAE GPAPAGTLPAPLFPSTYERLALLL GSIGLLGVGNLLVLVLYYKFQRLR TPHLLLVNISLSDLLVSLFGVTFTF VSCLRNGWVWDTVGCVWDGFSGS

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						LFARPAPLPARPRAPRPTPPRSPLAS STLPDPSRMAGAFLLRPLPPHAVQ DSIPVVSHLPPTCHQTLLPKMADN LPTEFDVVIIGTGLPESILAAACSRSG QRVLHIDSRSYGGNWFASFSGLL SWLKEYQQNNDIGEESTVWQDLI HETEEAITLRKKDETIQHTAEFCYAS QDMEDNVEEIGALQKNPSLGVSN FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVT DVEESVEKEK YCGDKTCMHTVSDKDGDGDKESKST VEDKADEPIRNRITYSQIVKEGRRFN IDLVSKLLYSQGLLIDLLIKSDVSRY VEFKNVTRILAFREGKVEQVPCSRA DVFNSKELTMVEKRMLMKFLTFCL EYEQHPDEYQAFRQCSFSEYLKTKK LTPNLQHFVLHSIAMTSESSCTIDG LNATKNFLQCLGRFGNTFFLFLYG QGEIPQGFCRMCAVFGGIYCLRHKV QCFVVDKESGRCKAIIHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQQTSLIVPPAE PGACAVRVTELCSSMTCMKDTYL VHLTCSSSKTAREDES VVKKLF YTETEINEEELTKPRLWALYFNMR DSSGISRSSYNGLPNSVYVCSGPDC GLGNEHAVKQAETLQEIFPTEEFC PPPPNPEDIIFDGGDKQPER/PLGTNN VVMAKLESSE\ESKNL\ESPEKHPSK LEKSNLEMLFWTSFMASEFSHLKD RFPI
2050	7547	A	2212	328	583	
2051	7548	A	2213	1	416	PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVYWPLFVLIFHAI SPIPHFIAKRVTYDS DATSSACRELA YFFTTGIVVSCLWISPVILARVALIK\ WGACGLVLAGNAVIFLTIQGFLLIF GARGDDFSW\EQW
2052	7549	A	2214	1	180	AAATGAVGAAIYPCAAPNWK*RND EKTAADYKILGGSVLHLVLALRGG GGLRQ
2053	7550	A	2215	162	557	VASEHSPKIGASQGLDYEPLL VVAK VWYLTRPTGTKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEIDIEP\ TDKVERNQRSVWEEKEGNPPPPQQQ RLHLQVAKQM\NDEKDSSLIYKILR WVQSFQT
2054	7551	A	2216	684	1496	LETSGLSENPLGQAVGFGQDEFFLE QTKKKGVKRPARLHTKP\SQAPAVE EAPSGA\SYNPSFEDHQTLSSAAHE V\ELQRQKEAEKLERQLRPCPATEQ ARHPRSSTFQELCEGLLEESDGE PGQGEGPEAGDAEVCSTPAR\LATT EK\KTEQQRREKA VHLRVRTARA ALRAA\RLRATQELVFRVRGIQRPQ V\ALRLA\ELARRRRRRQ\ARREAEA V\DKPRRLGT/RFKYQAPDIDVQL\SSE LTDLSRLTKPEGQHPSRPVQELPRG

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						GI
2055	7552	A	2217	116	285	KLRNQRIQERHTDGGPEPLKSL*CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA
2056	7553	A	2218	3421	3698	AGRGPLRLQSHRFGRRPSQVDCLSPA APDQPGQHKGKTPSPQKIQKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD
2057	7554	A	2219	381	1772	KMAESENRLQELSES\SQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGGDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFLREFHDIERKFAEMY QPLLEKRRQIINAIYEPTEECEYKS DSEDC\DDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDP\RGPID FWLTVLKNVDLTLPLIKKYDEPILK LLTDIKVKLSDPGEPLSFTLEFHFKP NEYFKNELLTkTYVLKSKLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LKTIKKKQKHRDL/WGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDDFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIHYDNWMAAI EEVKACCKNLEALVEDIDR
2058	7555	A	2220	17	250	
2059	7556	A	2221	2	899	GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSLATADLLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMA SLF\KKKTVDVKEQNR ELRGTRANRDRAALEKQEKQLEL EIKK\MAKIG\NKEA\CKVLAKQLVH LR\KQKT\RTFAVSSKVTSMSTQTKV MDS\QMKMAGAMSTTAKTMQAVN K\KMDPQKTLQTMQEFFGRENMK M\EMTEEMINDTLDDIFDGSDDEEE SQ\DIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\STSKATISDEEIERQLK ALGVD
2060	7557	A	2222	3	586	ARAMGISRDNLHKRRKTGGKRKPYP HKRRKYELGRPAANTKIGPRRIHT VRVRGGNKKYRALRLDVGNFSWG SECCTRKTRIIDIVYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPREEEIL NKKRSKKIQKKYDERKKNAKISSLL EEQFQQGKLLACIASRPGQCGRAD GYVLEGKELEFYLRKIKARKGK
2061	7558	A	2223	2	727	LFPASAEQMGISRDNW\HKP\RK TG GPRESPTYQAEKMSLGRPAANTK ILAPRRIQHSPVCRGG*QVNTVPLRF D\VGNFSGW/SKECCTRKTRIIDVV YNAI**PSWVRYRPLVERIC\VLID EQHPYRQWVRSPTYAL\PLGPQRK GAKLDSLRKEEIFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQGG KASLRCIAFK/RPGQC\GRA\DG YMT

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						RGHRVRSYYLRKIKARQSKINT
2062	7559	A	2224	298	408	CGII*ALNKKEHRGCDSPDPDTSYV LTPHTEEKYKKINEEFDNMMRNHKKI APGLPPQNFSMSVTVPVTPSPNALS YTNPGSS
2063	7560	A	2225	1	1369	
2064	7561	A	2226	409	1944	LKMGRKKIQITRIMDERNRQVTF TKRKFGMLMKKAYELSVLCDCEIALIIFN SSNKLQYASTDMDKVLLKYTEYN EPHESRTNSDIVEALNKKEHRGCD SDPDPDTSYVLTTPHTEEKYKKINEE FDNMMRNHKKIAPGLPPQNFSMSVT VTPVTPSPNALSNTNPGSSLVSPSLA ASSTLTDSSMLSPQTTLHRNVSPGA P\QRPPSTGNAGGMLSTTDLTVPNGA GSSPVGNGFVNSRASPNLIGATGAN SL\GKVMPTKSPPPPGGNLGMNSR KPDRLRVVIPPSSKGMMPPLSEEELE LNTQRISSSQATQPLATPVVSVTPS LPPQGLVYSAMPTVAYNTDY\SLTS ADLSALQGFNSPGMLS LGQVSAWQ QHHLGQAALSSLVAGGQLSQ\SNL SINTNQNISIKSEPTSPPRDRMT PSGFQQQQQQQQQQQQPPPPQPPQPPQ PPQPRQEMGRSPVDSLSSF\SSSYD GSDREDPRGDFHSPIVLGRPPNTED RESPSVKRMMDAWVT
2065	7562	A	2227	3	168	PCPTHSRMLGSPQPKRQLPVAPVPT AQP\PPSPPKGRCQGQEPKPPRLP SPAQGPW
2066	7563	A	2228	272	416	VGRCFLLSSGGFFSLTSALPPPS/ PSAHPGVLVTPFGAPTKPDRGRSRG
2067	7564	A	2229	109	866	DTRVGYFSSGAFAFFFLWARAECRP LSKDSL VKPRATLPSIVGLGSVAVP RARRARRQRERSRPRTGPGACLPPS LAPYGFARVERRARAMKAGFPVRR SGRKAPYGC GGMEVLALRCLAEHG HSLGG\SAALGAS\AAAARCKAAEA AADEPALCLQCDMND CYSRLRLV PTIPPNNKKVSKVEILQHVIDYILD LQLALETHPALLRQPPPPAPPHHPAGT CPAAPRTPLTALNTDPAGAR\NKQ GDSILCR
2068	7565	A	2230	107	1073	
2069	7566	A	2231	23	538	LPEVPHSLRPRVKPHLCCAQPAVRV MARLPKLA VFDLDYTLWPFWVD THVDVDPFHKSKVR*GQGLGAR*DP ARAERTLALSSDGTVRDRRGQDVR LYPEVPEVLKRLQSLGVPGAAASRT SEIEGANQLLELFDLFRCYLHSHPE WNESSNSKSRVRDICEGPNWAFEV QP
2070	7567	A	2232	685	1161	TFPLLPLADYTLWPFWVDTHVDPPF HNSR*GRDREDW/PAR*DPARAERT LALSSDGTVRDRRGPDVRLYPEVPE VLKRLQSLGVPGAAASRTSEIEGAN QLLELFDLFRYFVHREIYPGSKITHF

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						ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE
2071	7568	A	2233	79	564	SPTSAARSLRLRVMARLPKLAVFDL DYTLWPFWVDTHVDPFFHKSSDGT VRDRRGQDVRLYPEVPEVLKIDLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHR\EIYPGSKITHFERVA AEVTGISF\SQMIFDDEDERREYCRRSA NWCVTCTSHPEW
2072	7569	B	2234	48	209	XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX*
2073	7570	A	2235	2	353	
2074	7571	A	2236	3	676	SAVEFPPLSHTTGTRPRTPIQQE NGYFIHTLWMGLALLGVLDLSGQ HRRPRSPCQPNFQQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APATDGG\FNLTSTFLQEKTSVETR TML\LQPRGVPSASLQLTGVPHWGQ A/HYSVSVVETDYDQYALLY\TRAS KGPGEDEFMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDK CMTEQ
2075	7572	A	2237	1	1165	MGVTEVFLKDVITILLNLEELVQCRQ TWGEARTRGKRVLGSLADEIVVRT QPPSLEHKAWNATCKHWLAEEA ALEKYYLSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTLPLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFLTIFISIDRYL IIKYPFREHLLQKKEFAILSLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLLGFSVPLF VMCLFYYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFSVLFTPYHV MRNVRIASRLGSWKYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLLSFREK
2076	7573	A	2238	1	567	
2077	7574	A	2239	58	544	GKKMGSKAKKRVLLPTRPAPTVE QILEDVRGAPAEADPVFTILAPEDPP\ VPFRMMEDAEAPGEQLYQQSRAYV AANQRLQQAGNVLRQRCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGSATQAL PGGPSAPDWHSRGPSRGC
2078	7575	B	2240	1	1551	MCELDILHDSLYQFCPELHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLLGNRHLHKERL AVYRWHASFICSGNTMPIVLVDWS DIREQKRLMVLRASVALHGRSVTL YEKAFLPLEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSRSKGRKNQRSTRT HCHHPSPKIYSASAKEPWVLTNLP

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						VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFPDC DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSDQHANEFGLS WILLGARTPTCKADLSPRPYSCPHP QPQQRFLGDSGITTKSVPRYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLFPNRSPTWQ ISIDKGPRQDTFMLFPPIKI*
2079	7576	A	2241	2	456	GTRSTRTARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLLAAALLLL LLALYTARVDGSKCKC\SRKEPKIR YSDVKKL\EMKPK\YPHCEEKMMVIT TKSVSRYRGQEHCPHPKLQSTKRFI KWYNA\WNEKAQRRVYEEAQGLR RRIG
2080	7577	A	2242	308	615	ETRVASGTGAAEV*GMVRLDISE GRAAVAAVVGGVVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG
2081	7578	A	2243	332	484	
2082	7579	A	2244	240	610	LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVAAVVGGVVAVGTV\ PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS
2083	7580	B	2245	158	2382	MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPPG LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFMMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN*
2084	7581	A	2246	753	1007	LAQGCSPGPSQDTALPGPPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGNGSEGEKALTFHV CGDHPVKN
2085	7582	A	2254	188	833	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKL VFL\GLDNAGKTTLLHWLK DDQIGPTLFPPLPTSEE\LTIAG\MT\ FTTFD\LGGHGAKHVA VWN\YLPS QLMGFVFLVDCA\DHFSPSWNPKE LNALMT\DETILPMCPIL\ILGNK\IDR TDAISEEKLREIFGLYGQTTGKGNV TL\KELNA\RPM\EVFHVA VLLKEGK VYGRGFSAGLLPVLF
2086	7583	A	2256	333	621	CRKNSCYQAQNFNLRIPFSTTKLINL FHF*NDSQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFPSSL ESYIWHVKEKKYNPTAAAI
2087	7584	A	2257	29	659	LSVASFSFLSNASAEDTMSRLSRSL WAATCLGVLCVLSADKNTTQHPNV

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						TTLPPIVRETSAPVTPLPLVTTTPAPET CEGRNSCVSCFNVSVVNTT\CFWIE CK\DESYCSHNST\VSD\CQVGNTTD FCSVST\ATPVPTANS\TAKTHSSSP LLQLPRQLLHQGTTNNTVNS\TSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK
2088	7585	C	2258	101	411	MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQIPIKXXXXXXXXXXXX XXXXXLF*
2089	7586	A	2259	2	575	
2090	7587	A	2260	1	265	SDALSKAQNDVMEMKMQSERLSK EYDQL\AKEHSELQHSSFGFELSKRS HKNGSIGKQTGSRKGSFRKRQQEK TVNFIKDTLQYTVSK
2091	7588	A	2261	47	906	RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIFSFNVWGKIATFW NKAFLTIILLIVFLDAVREVRKYSS VHTIEKSSSRPDAYEHTQMKLFRS QKNLYIPGISLFFWLVLRLVTLITQ LAKEPVTQRCALYLQAENTNKA K\FMEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLTRELKTSDA L\SKAQNDVMEMKMQSERLSKEYD QLL\AKEHSELQVPLGSFYILAFAPGL HNPHSPSPRSGGFSIDNPRGALPP CLVCVLFHHL
2092	7589	A	2262	669	995	KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHIKSSKAIMTIPCKFISRKPWEG DCSSLEPHGVSAFDIWWPQLCIKKV LNHFSPRKN
2093	7590	A	2263	3	379	WPFLKLRLGTCGTCCSHEGRAAA WSAESSLQHSVVMTMSLPLNPKPFL N\GLTGKPMVMVCLKWGMKYKGYL VSVD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNNVLYIRGVEEEED GEMRE
2094	7591	A	2264	68	268	QYLSLLLTQYSLVFICWLFICL\LYV YLFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVLPFL
2095	7592	A	2266	190	554	HGVRSDLGRWPDHLCAVCRHYHH LLHLLLLLPLQDVPPTTSWLSPPHP PLWCM/PPYPQPPSVPPSYGPSLPG LPHHAASARECQHPYPIAVPTHLT HAHAHGPTTRPTTRPLAGRSSRD
2096	7593	A	2267	2	445	
2097	7594	A	2268	200	894	TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLKSGTSIPLHDHPG MHGMLKVLYGTVRISCMKLDAG GGQRPRALPPEQQFEPPLQPRREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPA AFLDILAPPYDP DDGRDCHYYRVLEPVRPKEASSA CDLPREVWLL\ETPQADDFWCEGEP

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						YPGPKGLPLKPLAHQERWAEDVPY PTTRAVSLPP
2098	7595	A	2269	257	781	QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPPIAFPPAFE AAQVEAKPDELKVTVKLKPRRLRAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPL\EDEID/EFSKE MGHFLKPDPGPKIIGKVWVWHEKGM NDK
2099	7596	A	2270	271	404	
2100	7597	A	2271	2	5684	PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEGQN LGPQAIPQDGSITHQISRPNNPFGP GFVNDQSRKQYE\EWQETQQLLQ MQQKYLEEQIGAHRSKKALSQKQ RTAKKAGREFPEEDAEQLKHVTEQ QSMVQKQLEQIRKQKQKEHAELIED YRIKQQQQCAMAPPTMMPVQPOP PLIPGATPPTMSQPTFPMVPQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPRVEFDDNNP FSESFQERERKERLREQQERQRIQL MQEVDQRALQQRME\EMEQHGM VGSEISSRSTVSQIPFYSSRLYLCDF VMQPLGLPQQSPQHQQQMGQVLQ QQNIQQGSINSPSTQTFMQTNERRQ VGPPSFVPDSPSIPVGSPPNFSSVKQG HGNLSGTSFQQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGGKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELQQADQESVEPV GPSTPNMAAGQLCTELENKLPNSDF SQATPNQQTYANSEVDKLSMETPA KTEEIKLEKAETESCPGQEEPKLEEQ NGSKVEGNAVACPVSSAQSPPHSA GAPAAKGDSGNELLKHLLKNKKSS SLLNQKPEGSICSEDDCTKDNKLVE KQNPAGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNSGNRLLGTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQGPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLSLVKE EPPEPVPSPIIPILPSTAGKSSESRRND IKTEPGTLYFASPFGPSNNGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHCKVVILG

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						SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFFKPCDEIDEFL KKLGTSLKPDVPVKDYRKCCFCHEE GDGLTDGPARLLNLDLWVHLNC ALWSTEVYETQAGALINVELALRR GLQMKCVFCHKTGATSGCHRFRCT NIYHFTCAIKAQCMFF\KDKTMLCP MHKPKGIHEQELSYFAVFRVYVQ RDEVQRQIASIVQRGERDHTFRVGLI FHTIGQLLPQQ\MQAFHSPK\ALFPV GYEA\SRLLLGTRYANRRCR\YLC SIEGGRDG\RPVFVIR\IVGNKGHGR TGV LKVD\SPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFLTVS AVARIAESLPGVEACENYTFRYGRN PLMEPLAVNPTGCARSEPKMSAH VKRFVLRPHTLNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMKT\ EWKSNVYL\ARSRVSGGWGLLWL VVRTLEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMFMRMDN DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKDFDQHKIPCHCGAVNCR KWMN
2101	7598	A	2272	1	2806	
2102	7599	A	2273	288	843	AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPIKSRK\GD VLHMHYTG\KLEDGTEFDSKPAPR TSPFVFSL\GTGQVIKG\WDQG/LCL GMCEGE\KRK\LVIPS\ELGYGE/RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKKTLSKPK
2103	7600	A	2274	80	308	VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWHA
2104	7601	A	2275	2	456	RSFFFFCEVGSWVGSMRVVMARL LSEGEQGIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLFL VSLGTDLARGRGNSASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QGWVSTSWGSSSPVQFFPKLLEF TGK
2105	7602	A	2276	2	81	
2106	7603	A	2277	325	485	ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLTS KYR
2107	7604	A	2278	291	529	LFLLCVGTWHQGPNHQKAPKAPG TPPTPSYPGTPSRQLLWQWVQPRPA LPA\LPVAVGTSSTSPGRQCPGSAQ HHLFP
2108	7605	A	2279	52	109	TVRLPR\HPGSRKNMASYCRIPACIA AERRYGTCTMYQGRIWAFSS

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2109	7606	A	2280	3	452	
2110	7607	A	2281	26	526	NSTDSE RTHPWLLSPADKTTVK/AP AWGKVG AHAGEY GSEALERMFLS FPTTKTYFP HFDLSHGFCPLRATG KKVADALTKRRGAPLDDMPNALV RPL\SDLHA HKL\RVGPGSTFKLLKP LACL\TLGPAHLPRPSFTPGGCKAS LGQSFLGFL LKHRCNLNPNYR
2111	7608	A	2282	447	539	
2112	7609	B	2283	8	694	MQYNRRFVN VVPTFGKKKGTTFTK IFVGGLPYHTT DASLRKYFEGFGDIE EAVVITDRQTG KSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVVI PAA PVPSLSSPYIEYTPASPVYAQYPPAT YDQYPYAAS PATADSFVGYSYPAA VHQALSAAAPAGTTTFVQYQAPQLQ PDRMQ*
2113	7610	A	2284	3	191	
2114	7611	A	2285	101	444	CSLFVPRPRSLQPLRRVTGQETGRP RSKAHVASTWRAFPPEQV VLLAG AP\LEDEATLGQCGVEALT TLEVTVG \RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG
2115	7612	A	2286	2622	2881	KKSKDNKTFFFFFETESCSALQAGV QWCNLGSLQTLPGSND SHASASR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGTPDLK
2116	7613	A	2287	41	655	TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAE\STKIPR L\RTDLFPKTRIQ\DLN\RIFPLSEDYS GSGFGSGSGSG\SGS\GSWFPNGKW EQDYQL\VDE\SDAFHDNLR\SLARI LASASRDWGQHGLAEFNVIKEDL PTLTTRQMVVKQYFNVPMVNMINS WDKEFYRNF
2117	7614	A	2291	163	703	READMGTMKTQRDGHSLGRWSLV LLLLG\LV MPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDP RPT MDGGP\DTTK\PVSFTVKETVCPRP TQQ\SPKDGDFKRDGLLN RGMGTV\ TLN\QARGSFDISCDKDNKR FALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPRTES
2118	7615	A	2292	100	546	PPRTGQRQPLHSARRHG PSVS\ELAC I\YSALISARTDEVTVT\EDKINAL\IK A\AGVNVE\PFWPWLCLQRPLA\NV NIG\SL\CNVRGPVEPAPSSLVAAP\ AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL
2119	7616	A	2293	33	494	
2120	7617	A	2294	1	609	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVD EVGGEALGRLLVVYPWT QRFFESFGDLSTPD AVMGNPKVKA

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						HS\KKGLRGAFSDGLAHL\DNLKGT FATL\SEL\HCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN
2121	7618	A	2295	1	338	AALAWAVSRLHFSRLSFPPWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNV FFPVVDGFIRRVPLVLSLLNLPGIRS FVDKVGESNNMV
2122	7619	A	2296	67	283	LPFPGCIFFLF*VLFVAGLAFVIGLER TFRFFFQKHMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR
2123	7620	A	2297	3	209	
2124	7621	A	2298	3	544	TRAALAVAVSRLHFSRLSFPPWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAF\VIGLERTFRFFF\QKH KMKATGFFLGWVYL\VLIGL/WPLI G\MIFEIYG\FLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVGES SNNMV
2125	7622	B	2299	54	1731	XKLSRECEIKYTGFDRDPHEERQAR FQNACRDGRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLERA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLEVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERAAAAKKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDRVRKATQQAE QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEVEQEAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNA RVKQLKRQLEEA EESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPQETSQ*
2126	7623	A	2300	1	2448	
2127	7624	A	2301	1	2655	
2128	7625	A	2302	5	605	VDPDSGQIQVPCTPRGLKWSNMN PARKTDACGEDTHPSLLGVPSRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLRSQRPAPPPQE PKMPSLCCRNTSTTFSGRPSQSPRTK KQRPR
2129	7626	A	2303	1	588	MGFCHVDQTGLELLTQPLLALIGAA

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						LEGGRAGGAADLAPDFGRLALQIK YTGFRDRPH/EERQARFQNA CRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPNLVTPPRYTP MVPCGGHHQAQRKRPLCTPPSSIQ QGSMSVKSMPTPVA AHKSFTSALC
2130	7627	A	2304	1	615	GLKGGKMPRVVPDQRSKFENEEFF RKLSRECEIKYTGFRDRPHEERQAR FQNA CRDGRSEIAFVATGTNLSLQF FPASWQGDQROTPIREYVDLAREA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTQ QAFEEARRMTREFEDRDRSHRQEM EARVSQLLAVTGKK\QLDPRPGSNL GGGDDLKLR
2131	7628	A	2305	73	168	
2132	7629	A	2306	322	671	RLWASPAAPGKKKEMGNSMKSTP APAERPLPNPEGLDSDFLAVLSDYP SPDINPPIFRRGEKLRVISDERGWW KAISLSTGRESYIPAICVARSYHGW LLRPG\KNMAEELLQLPD
2133	7630	A	2307	624	1581	KAATSENKIIICEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLPNPEGLDSDFLAVLSDYPS DISPPIFRRGEKLRVISDEGGWWKAI SL\STGRESYIPG\ICVARV\YHGL/W LFEG LGRDKAEELLQLPDTKVGSF M\RESETKKGFYSLSVRHRQVKTY RIFRLPNNWYYISPRLTFCCL\EDLAV NHYSEVADGLCCVLTPCL\TQSTA\ APAV\RACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSPPYFED
2134	7631	A	2308	52	454	SQTQREPTMVLSPADKTNVAAA/W GMFLSFPTTKTYFPFHDLSHGAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKL RVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLTSKYR
2135	7632	A	2309	3	452	
2136	7633	A	2310	26	502	NSTDSE RTHHGARLLPDKTKAQRPP RLKLGANA\GEYGF GGPWKGMFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DAL TQSPCRNVD\DM PQ TALSAP EATLHG\HKL\RVDPVNFKL \LSH\CLLG*PWP AHLPRPSFTPCGCT PSLEQSSW AFC
2137	7634	A	2313	43	595	LRNMWQLERN\IET\IINTFHQYSVK LGHP\DTL\NQGEFKELVRKDLGQN FLKKENKNEK VIEH\IHEDLDT\NAA Q\QLSFEEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGHKSWWPRQA TNHGGQATLPLPKPGPRGLLCQTVL AVGLGGWGQIKSLP

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2138	7635	A	2314	3	419	SLYHNSSQKRHWTFSSSEQLARLRA DANRKFRCKAVANGKVLNPDPVFL EPHEMTLCKYYEKRLLEFCSVFKP AMPRSVVLTCAFLACKVDEFNVSN PQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN
2139	7636	B	2315	324	487	MQRVRAGRIVITTAQRRLPDALG FREIFSSEEQLARLRADANPNSSDAK PWPTGS*
2140	7637	A	2316	1	1050	
2141	7638	A	2317	191	229	
2142	7639	A	2318	186	1232	CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRK\FR CKTRAH\GKVFPNDPVFLEPHE\EMT LCKYYEKRVIE\FCSVFKPAMPRSV VG\SRACMYFKRFYLNNSVM\EYHP RL\IML\TCAFLACKVDEFNVSSPQF VG\NL\RESPLG\QEKALEQILEYELL PYTSNFNHFLI\VNHPY\RPFEGFL\ND LRTR\YPILNPEILRK\TA\DDFLNRI ALTDAYFLYTPSQ\IALTAILSSASRA GITMESYLSLMLKENRTCLSQLL DIMKSVRN\LKKYEP\PRSEEVAVL KQKLERCHSAELALNVITKKRKG EDDDYVSKKSKHEEEWTD\DLV ESL
2143	7640	A	2319	152	371	DVLLATSSSEPSLFCPLCLTASTPKP LPPPG\PLPCPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS
2144	7641	A	2320	4	474	PQYPAWHEGERAEWLCGRVSETGS ACSMADQL\TLKEQIAEFKEAFSL\F DKDGDGTITTK\ENLGTVNEILLGSN PTEAELQDM\NEVDADGNGTIDFP\ EFLTMMARKMK\DTDSEGRKL\EEA F\RVFGLRVGNGLYL\ACRNFRHV DGQTLGGSLPD
2145	7642	A	2321	291	648	LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHRSPSTSTSPF GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRAS\HPAGPPVPPSGVLV SRRRPEPGQGKPPESDFDH
2146	7643	C	2322	155	316	MTGPVSGSFIHWVLFSGFSSMSSNA SNVFGLVRPSCCTGLSRMAADSAG CCSL*
2147	7644	A	2323	28	1323	PSGARVAGAGPCGGGGMFVQEEKI FAGKV\LRHLICASDGAEWLEEATE DTSVEKLKERCLKHCAHGSLKDPK S\THHKLIIHAASERVLSDARTILEENI QDQDVLLLIK\RAP\SPLPKMADV AEEKKK\QDQKAPDKEGILG\ATAN LPSNKLDRAAVQTNMRDFQTELK ILVSLIEVA\QKLLAL\NPDAV\ELFK EGECNCWDEDGGMSVWDEACPAA FQREMGLFRENRTAKALQLNHMS\ VPQAIGSWLI\EHAE\EDPTIDTPL\PG\ QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRKREFRADA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RAVISLMEMGFDEKEVIDALRVNN NQNAACEWLLGDRKPSPEELDK GIDPD\SPL\FQAIWDTRWVQLGLTN PKTLAFEDMLENPLNSTQWMNDP ETGPVMLQISRIFQTLNRT
2148	7645	A	2326	307	412	SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE
2149	7646	A	2327	50	247	
2150	7647	B	2328	276	779	MRTLAILAAILLVALQAQAEPLQAR ADEVAAAPEQIAADIPEVVDSEFAW DERAPLQVSGKSSPVCARLLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMPL HGMKVPLFRFQPDKIIVLSTLIPTGD YSPHNLKNLFMRMVTPSP*
2151	7648	A	2329	3	333	
2152	7649	A	2330	35	717	RRSSPSLLPLAERGGRARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVS\SSR\HPDRWVPWKEG MEARRKEAKCGKQVREVCEGRLG VKGT\LGRLVGIF\ENQERKH\RTYV\ YVLIVTE\VLEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTP\VV\ATTYSVSGFRA SMFRAFRWT
2153	7650	A	2331	104	381	IQGGSMTTSSSFSTICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS
2154	7651	B	2332	228	445	METSSRELQAAEYLEKHQIKEVVS YLTSAALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX*
2155	7652	A	2333	3	1459	GSKQVSEGTNDGDLPSYVSFAFIEKE VGNDLKSLLKLDKLEIQRVTSKMQ LEEQVLTISSEIPKRIRSALKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISSQIEEIERHLAYLKWI SQIEELSDNIQQYLMTNVPEAAST LVSMALDIKLQESSCTHLLGFMRA TVKFWHKILDKLTSDFEELAQLH WPFIAAPPQSQTVGLSRPASAPEIYSY LETLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTPLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGS LVNARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMLSSEAAWVSQ YKDITDVDEMKVDPDAETFMTHLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK
2156	7653	A	2335	46	1146	
2157	7654	C	2336	17	196	MTTLVTTTTMDMVIIATSRVVMGR YPGEVVIKIATNHTKLFHLQLIPNSG NFIAGPVS*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2158	7655	A	2337	208	1504	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSASEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLDPITGRSRGFGFVLFKESESV DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEVESIELPMDNKTNKR FCFITFKEEEPVKKIMEKKYHNVGL SKCEIKVAMSKEQYQQQQWQWSR GGFAGRARGRGGGPSQNWQNGYS NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSN\SQSGYGK VS\RRGGHQ\NSYKPHLNY\NICNL\S PTGGEAVFS\NLKIQFESGS/CH*LLI AVQTKF\LYQVPEWKYD\VGSL
2159	7656	A	2338	208	1466	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSASEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLDPITGRSRGFGFVLFKESESV DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*G\EEPVKKIMEKKYHNVG LSKCELK\VA\MSKEQYQQ\Q\QQW DSRGGCAGRA\RGRGGDQ\QSGYG K\VSRRGG\HQ\NSYKPYLNY\NICNL SPTAGTSLQALCRADFRFSQARSMR TG*RDAPRSRMLPFGGEAVFS\NLKI HL/NGGSCHLLIAVQTKFLYQVPE WKYDVGSL
2160	7657	A	2339	1070	1238	PQRDFQFFLLWPPGGEA\VFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL
2161	7658	A	2342	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALERMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNVGHVDDMPNALSALS DLHAHKL RVD PVNFKLLSHCLLV T LAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR
2162	7659	A	2343	2	512	GLEFGTSHRLRENPPWCLSPA\DKT NVKAA\WGKVG AHAGEYGAEALERMFL SFPT\TKTYFPHFDLSHGFAQ VKGATAKKVA\DALTKAVAHRGRT CPN\ALSALSGPATAHKL RVGPGST FKLLKPLACLVDPGPAHLPRPSFNP WRLQGFLGTFKLGFLVEAPLLEPSK
2163	7660	A	2344	265	426	SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMHAHTWPLCLQDVLV ECCSQS
2164	7661	A	2345	56	341	IVTLDWSRNLKYNRCWSKCYILSSS DSSSSFRDSFTNPAEF*FKSFILNFV

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						MYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV
2165	7662	A	2346	333	534	LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FLL\HPM*LFSPGLYILSNFH
2166	7663	C	2347	117	386	MDILICTDFGSVNYFNVWRLPKSYL SLFYSRIYIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREEAKEYAK ESLKEEDESDDDNM*
2167	7664	A	2348	2	359	FEDGVLLCHPRLESGT\ISAHCNLS LPGFKRSSCLRLP\SSWDYRNMPPY PGYFCIFGFTNNTETGFHQASFLL NSRDLPTLAPVKCWDYRHEHCTRP LKYIFYQRYSHCMLEQHLLN
2168	7665	A	2349	648	887	SWKLLLLLCLLKNEHLPTKPATGHS NIADQTLKKSFCLEPFFHKV*KGLIF LTPRTTPSLHLPIAVLLFSTAFIAYS T
2169	7666	A	2350	306	449	EIKKKYLLPGVVAHACKPSTLGG GGQIISGQEFET\SLTNMAKPCFF
2170	7667	A	2351	1	625	NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWGK\VNVE\DAAGGE TPGKGSLLVYP\WT\QRFFDSFGNLS SAFCPSWPTPKVKAHGK\KVL\TSLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK
2171	7668	A	2352	1324	1671	IVQTLSTLSKSSCRSTEPCTSCLPDLP QVGTTCRPHGTCC/NRCHVGGLMN PLKPNC/GCRKCNCGYLYIYLKGQR LHPRGKFQPGNNHRFSCTQSVHMDI THGSGMFSLCFPGSTMF
2172	7669	A	2356	8	564	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPEEKSAVTALWGK VNVE\VGKALGRLLVYPWTQR FLAES\FGDLSTPNAVMANPKVKAHS \KK\LGALLVVGLAHL\DNLKGTFA HTEVSLHCDKLH\DPENFQAPGAT CLVLCAWANHFWQKNFTPPV\QAC LFRKLVAG\VANALAHK
2173	7670	A	2357	23	679	GLLTSGGAHLSPSRVTQGIYMSAL SEMPKPPDYSELSDSLTAVGTRGF SGPLHRAWRMNFRQRMGWIGV GLYLLASAAFYVFEISETYNRLA L\EHQQHPPEPLEGTTW\THSLKAQ LLSLPFW\WDSYFFWVPY\QMFF VSLYSCYKELDPQNSGGYCYPSPIW LWAVYFGNRHHAF/VVKASNSDSA DLQLIDTVKSVTRFFPLRITKTGQS
2174	7671	A	2358	17	392	SFKMADQDPAGMSPLQQMVASGT GAVVTSLFMTPLDVVKVRLQSQR SMAS\DAFVKIVRHEGRTLWSGLP ATLVMTVPATAIYFTAYDQLKAFL CGRALTSPLYAPMVAGALARREHR LGPLTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2175	7672	A	2359	1	725	RFTGTMDAFVKIVRHEGTRTLWSG LPATLVMTPATAIYFTAYDQLKAF LCGRALTSPLYAPMVAGALARLSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLELMR TKLQAQHVSYRELGACVRTAVAQG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVA AELTLPY
2176	7673	A	2360	102	1573	SFKMADQDPAGISPLQQMVASGTG AVVTSLSFMTPLDVGKVRLOQSVQPS MASELMPSRLW\SLSYTKLPSSLQS TGKCLLYCNGVL\EPLYL\CPNGAR CATWF\QDPTRFTGTMD\AFVKIGE ARGAPRTLWSGLPATLVMTPATA IYFTAYDQLKAFLCGRALTSPLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVRNRELGACVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPQAL\YWFNYEL\VRSWL\NG LRPK\DQTSVG\MSFVAGGISRTVA AVLTLPF\DVVKTRQO\VALGAL\EA VKSEPPCNVDST\WLL\LRIR\AESG TKGTLLQASFPRIKGCPPSCA\IMIQ HLIEFRQKAFFPRGLNPGTGFLGGL EKGPKGKDPVSSQREWGGRGQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSPGRSTSSRHNFLLPVVGI ITYPPPKFKTKSSELPFVFPCGLL
2177	7674	A	2361	1	215	QPMSEEEEDQYLA VLTFFRCVLV MIHTHAQVLNHVCIYVCVHMSVA V Y/ISACRATDPDTHTCVYMIQTY
2178	7675	A	2362	3	543	TRNTLGWEVSSFSPLLSCLNMVRT KADSVPGTQEKVVAARAPRKGVLG SSTSAHLIRPSVSIEESLKNKYARRE PPFCVRP/TLPKWAKREIGEFFRLSP KDSEKENQ\PEE\AGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTFLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG
2179	7676	C	2363	69	290	MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDGWQPFLLSAGER*
2180	7677	A	2364	663	793	DGDSVMVLPTIPVEEAKKLFPGKGVF \TKELPFGKKYLRYTPQP
2181	7678	A	2365	1	726	MPGGLLLGDVAPNFEANTTVGRIRF HDFLGDSWGHSFSQP/RGGFTPWCA PRSFARA AKLAPDFAKR\NVKLIAS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLFP\PIIDDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCFVFGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMVLPNPSPPEEEA\KKLFPEKE SFTQKELPNLAKKYL\RYTPQP
2182	7679	A	2366	3	452	
2183	7680	A	2367	1	627	TLLVPQDSERTHPWLLSPADK\TNV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KAAWGVGAHAVRSMCAEALER MFLSFPTTKTYFPHF\DLSHGSAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKL\RVGPGST SKLLKPLACLVDPGPAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPPAPPP LSCTRTPVVFEIKS
2184	7681	A	2369	1	467	GTSACGVASLSVVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNYLCIRA ASSQHLKCHWVGGNKTCFGPDDLF GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM
2185	7682	A	2370	131	406	EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATQRLANF L\VHSSNNLGGILSSTNVGSNTY GK RNAVEVLKREPLNYLPL
2186	7683	C	2371	257	422	MQVCFRQGF\LPKGHHGLIATLGA PQLYMFLVLRASLFLWLSXFXRSX KLXXXRN*
2187	7684	A	2372	621	1202	GVPEPRARPSTSGMNGDRIRLPCWR NDRQK\THML\DV MQDHFSRASSIH RRALSRDRFFTREPQ\DT\YHYL\APFQ PCPHRRP\HFFFPKSRNRPA*\CPFSS \TKPLNFHAMFQPFLEMIHEGSAGP WDIHFHSPAFQHPPTFEIREGD\DDR DCCAGE\IRHNSTGLPCGLKDQVVT K\CREDLVLWDCFHQQLPG
2188	7685	A	2375	154	1702	IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAG\VSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIQAKTS PVDEKALQDQLVLVA AKLDTEK RAAMV\GMLANFLGFYYMGMS E\WGV\VHG\ATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSR\DAHKVLSAL\QAVTGLLVA PGRADKQA\QLL\LSTVVGVTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETID\RLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGKM KGFSLLAEPQ\EFWVDNSTSVSVP LSG\MGTFQHWSDIQ\DNFSVTQVPF TD\SAFLLLIQPHYASDL\DKVEGLT FQQN\SFNWMRKLFPRTIHLTMPQL VLQGSY\DLQDLLRPGSSCPFLHTE LNLGRISGN\DRIRVGEVLNSIFFEL EADEREPTTESTQQLNKP\EVLE\VP TRPFLFAVY\DQGATALALSWGRV GKPA
2189	7686	A	2376	181	353	VGDRCEGNGNEARGHWKREVCCP GARSGASV*GSSGRLGLCL*VGTR AG*PGYPASLVPT
2190	7687	A	2377	1550	1823	GRLLEDPAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFPPNLEKTVTFQSLLGPLKIPKEPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKEIKLTNVKSKSTLP
2191	7688	A	2378	134	321	GCF*KGRDLFADKMQEHSQ*FTAL FQPTNQKISSWVCGPKVNFKAIKTG SRSGKAIQNVES
2192	7689	A	2379	1	602	RTRASTRPSRDYGNVWLWTRTSHP RPLTEPEPRATMSHGKGTMDLPEIA AP\VGFLSSLLRTRGCVSEQRLKVFS GALQEA\LTEHYNHHWFPEKP\SRG SG\YRCIR\NHK\MTPIISRVASQ\VG LSQAQL\HQLLP\SELTLWVDP\YEV S\YRIGEDGSICVLYE\EAPLAASCGA SFT\CARNQVACWGRSSPSK\NYVM AVSS
2193	7690	A	2380	28	423	SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCIV*M STSKTGKHGHAKVHLVGIDIFTGKK YEDICPSTHNMDVPNIKRNDQFLIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG
2194	7691	A	2381	1	930	
2195	7692	A	2382	171	695	NRQDDLDFETGDA\GASATFPM\QC SALRKNGFVVLKGRPCIVEMSTSK TG\KHGHAK\VHLVGIDIFTGK\KYE\ DICPSTHD\MDVP\NIKR\DFQLIGI QGWTLSL\Q\DSGEVREDL\RVSP EGDL\GKEIEQKYDCGEEILIP\VLSA\ MTEEA\VAIKAHGKITGSPGVAVV ASK
2196	7693	A	2383	789	1380	IPYFLMVYGLQTLMCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPIPPQKKDYWVLLSLGAPKFK GYLVLCMLQEPCKRQPGKSTGWI RNYPWSMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWGSPGQEQVLGLQ
2197	7694	C	2384	248	433	MSGILVLNLFLLTGLSVGPSSSVTLV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP*
2198	7695	A	2385	1	1108	
2199	7696	A	2386	1	1528	MGTRAARPAGLPCGAENPARRRLA LGARQQIHSWSPRTPTSTRLTAPAGP ARGVARPAMAPDPVAAETAAGQPT PRYFTWDEVAQRSGCEERWLVID\R KVYN\INEFTRRHPPGGSRVISHYAG QDATDPFVAFHINKGLVKKYMNSL LIGELSPEQPSFEPTKNKELTDEFRE LRATVERMGLMKANHVFFLLYLLH ILLLDGAAWTLWVFGTSFLPFLLC AVLLSAVQAQAGWLQHDFG\HLS VFSTSK\WNHLL\HHFVIGHLKGAPA SWRNHMHFQHHAKPNCFRKDPDIN MHPFFFALGKILSVELGK\RKKKFM PYNHQHKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRFF LTYVPLLGLKAFGL\LFFIVRFL\ESN WFWVVTQMNHHPMHIDHNRNM\D

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WVSTQLQ\ATCNVHKSC/AFNDWV SVG\HFNQIEHHLFPTMPRHNYHK VA\PLVQSLCAKHGIEYQSKPLLSAF A\DIHSLKESG\QLWLDAYLHQ
2200	7697	A	2387	45	949	APWWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGR SSAPAHGDESCSLPRPLSLAHGEP GRRRAEACSRLSRSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQSRSEAQPDPAEQ PRKRW
2201	7698	A	2388	804	985	VGGDSQDLRDPVPPQTAPPPPNLS PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG
2202	7699	C	2389	258	461	MSVTFIAVARGKLFFENLGHSELPL SLEWQTSDEGEVEARGSRGGEALPR PGSMQPCPADVTRPPTRP*
2203	7700	A	2390	1	370	GTRVTSGGGSRRPGMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQ\ILKRKVSRLQLIKVTDISGG CGA\MYEIKIESEEFKEKRTVQQHQ MANQALKEEIKEMHGLRIFTSVPK R
2204	7701	A	2391	1	1107	
2205	7702	A	2392	1	1230	
2206	7703	A	2393	1	908	
2207	7704	A	2394	177	934	PGLSQEPSGSMETVVIVAIGVLATIF LASFAALVLVCRQR\YCR\PRDL\AQ RYDSKPIV\DLIGAM\ETQSEPSLE LDDVVITNPHIEAIL\EN\EDWIEDAS GLMSH\CIAIL\KICHTLTE\KLVCHD NGALGAKMKTSASVSDIIVVAKRIS PRVDDVVKSMYPPLDPKLL\DART\ TALLSV\SHLVLVTRNACHL\TG\G LDW\DQSL\AAEEHLEVLREAAL\ ASEPDKGLPGP\EAFLQEPVLQFSAY RPAA
2208	7705	A	2395	1	333	GTRGERKAGLARGQVCGLSPFPK TNKESFPNSQLNPFWN\Y\CGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDNDSRLLSRMTSMCSISR VPEHVEFPNPK
2209	7706	C	2396	7	279	MXKGSXPXNFLECEKKSGQNPWAG LLRPWWVGHPSAKPLIPVFSSISFPL YNPHFPIXILCNKLKSHVCKKASKY TNNPISQQWTLFSIK*
2210	7707	A	2397	35	416	SRAVEFVRSCAGYGERKAGLARGQ VCGLSPFPKTNKESFPNSQLNPFW\ NYVWGLGPCGASLSL\VSFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSR\MTSMCSISRVPEHVEFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NPK
2211	7708	A	2398	3	344	
2212	7709	A	2399	1	1359	
2213	7710	A	2400	1	463	LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCRAGTEDEEEEE GRRETPEDREVRLQLARKREVLLR RQTKTSLEVSLLEKYPCSKFIIAIGN NAVAFLLSSFVMNSGVWEEVGCACL WNEWCRITDTHLSSTEAFVCFYH LKSNPVFLCQCSCYVAEDQQYQW LEKVF\GSCPRKNMQITILTCRHCT\ DIKTSESTGSLPSPFLRALKTQNF\K DSACCPLEQPNIVHDLPAAVLSYC QVWKIPAILYLCYTDVIGLDFITVE AFKPILSYR\SLKGLV\KNIPQSTEIL\ KKLMTTNEIQSNIYT
2214	7711	A	2407	160	441	
2215	7712	A	2408	107	691	RTAILSRMKIFLPVLLAALLGVERAS SL\MCFSCLNQKSNLY\CLKPTICSD Q\DNV\CVTVSAS\AGIG\NLVTFGH SL\SKTCFPCLAPFPEGRSMLGV\AS MGHSAFCQSFLVAIFSCGPMAGLRG KRSPLLGARACCLSLAGRALL\RFG PLDRPEPCSPDPPAQEGKSPFWIPQ CMGAPDSSRALICALGPRSG
2216	7713	A	2409	2	432	GRPPPDVEVMTSLKVDNLTYHTSP DVYIPRDRYTKESRCFAFVRFHDKR DAEDAMDAMDGAVLD/GSELRLQ MARYGRTPDSHHSRRGPPPSYGC VGYGRRSRSPRLRRMP/RSRSPRSR SRSPRSRYSRSKSRSTRSRSRSTS
2217	7714	B	2410	1522	2003	MAIIYGVSASNLITPSVVAIVGPQL SMFASGLFYSMYIAVFIQFPWSFY TASVFIGIAAAVLWTAQGNCLTINS DEHSIGRNSGIFWALLQSSLFFGNLY IYFAWQGKTQISESDRRTVFIALTVI SLVGTVLFFLIRKPDSENVLGEDESS DDQDMEVNESAQNNLTKAVDFAK KSFKLCVTKEMLLSITTAYTGLEL TFFSGVYGTICGATNKFGEESLIG LSGIFIGIGEILGGSFLGLLSKNNRFG RNPVVLGILVHFIAFYILFNMPGD APIAPVKGTDSSAYIKSSKEVAILCS FLLGLGDSFNTQLLSILGFLYSEDS APAFKFKFVQSICAAVAFFYSNYLL LHWQLVMVIFGFFGTIFFFTVEWE AAAFVARGSDYRSIMLKSFLDSGDI LAQLCRRQQPRAPLTIRTSPTDLRR VFEKYGRVGDVYIPRDRYTKESRGF AFVRFHDKRDAEDAMDAMDGAVL DGRELRVQMARYGRPPDSHHSRRG PPPRS*
2218	7715	A	2411	2	229	
2219	7716	A	2412	3	353	FPLPFFTLVIWPGIRKFKLVHADGSL CEIFLIGPFKNMAGWNISVPYWFDQ SLSKYVPETETMCTLMGKLNFFLF KPRCIGKQCKRRTWGKRTT*SIRRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SPWNKQLGYLKRLFW
2220	7717	A	2413	18	282	DPLKSGPRNRS*TRWTPSPRS\ARRS KSKSLSVSRSRSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSPSP\EE EAGVLLRK
2221	7718	A	2414	2	830	LRSPSVLFCGKAFFVSPRGRQLPER RGVAPPRAEEAGASSRSGPPLRA MSYGRPPPDVEGMTSLKVDNLTV\ RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFHDKRDAE DAMDAMDGAVLDGGELRVQMAR YGRPPDSHHSRRGPPPRRYGG\GY GRRSRSPRRRRRSRSRSRSRSRSR SRYSRSKSRSRTRSRSRSTSKRSAR RSKSKYSSVSRSRSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSS\EEGA VSS
2222	7719	A	2415	1	320	RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSHTAKEP YTRNECGKVFG/HIARHQIHHSTKEP YKCN/NTLKAFSKHSGLMAHLLIDR PEKLCHYS
2223	7720	A	2416	733	1005	NPQTPMKNCWPLEKKAEP RPFLGS SMPLGFCHPGPPCSCDFLETHFLDE \EVKLIKMGDHLTN\HR/LGDPEA GLGEYLFERLTLKHD
2224	7721	A	2417	148	1057	
2225	7722	A	2418	87	241	EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC
2226	7723	A	2419	1	924	
2227	7724	A	2420	1	1004	MPVGAGRRRAKGD PATLGALAVFTV GAKRSKGHSPKPHPAGRLPPLPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLMDCRPQEL YESSHIESAINVAIPGIMLRRLQKGN LPVRALFTRGEDRDRFTRRCGTDV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGFSKFQAEFS LHCETNLDGSCSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSG SPLSNSQPSFPVEILPFLYLGC AKDS TNLDVLEEFRGSSPYMILFHYGENIG TSYVPITSHFRQKLAQGFPVSTGTP GFIYSAK
2228	7725	A	2421	686	1812	TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGFSKFQA EFSLHCETNLDGSCSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQPSFPVEALALPSYLG C AKDSTNLDVLEEFGIKYILNVTPNL PNLFENAGEFKYKQIPISDHWSONL SQFFPEAISFIDEARGKNCVGVLVHCL AGISRSVTVTVA YLMQKLNLSMND AYDIVK\KKKSNISPNFNFMGQQL GLSRRDAGDSAGPCGQQGSRHSRL YFYHPFPTRNVLPGWDFLQSTWKD

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						PTPFLAGMCLALQQFLLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG
2229	7726	A	2422	66	187	WGGGGSAAAAMEANWTAFLFQAH EASHHQQQAAQNSLLPLSSAVEPP DQKPLLPIPIQKPGAPETLKDAIGI KKEKPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTTSS SGTNPSSSASTTAMPVTQSVKKPASK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPCINQRFKRKDR MTYHVRSHGEGITKPYTCSVCGKG FSRPDHLCHVKHVHSTERPFKCQT CTAAFATKDLRLTHMVRHEGKVSC NICGKLLSAA YITSHLKTHGQSQSIN CNTCKQGISKTCMSEETSNQKQQQ QQQQQQQQQTHVTSWPGAKQVET LR\LWEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSGTMSNP VTVAAAMSMRSPVNVSSAVNITSP MNIGHPTITSPLSMTSPLTLTTPVN LPTPVTAPVNIAHPVTITSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSP\WRPTGPRSCSRPMKLPITNSR QHRTACCPs
2230	7727	A	2423	3	777	RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFGLSPTVVTLAEL LVLLAALLATVSGYFVVIDAHAEEC FFERVTSGTKMGLIFEVAEGGFLD\I DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYKF\CFSN\RMSTMTPKI\I VMFTI\DIGEAPK\GQD\METEAHQN KL\EEMINELAVA\MTAVKH\EQEY MEVRERIHRAIQRTTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG
2231	7728	A	2426	89	136	
2232	7729	A	2427	1	916	MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQKEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSPQARE DQLQRKAVVL\EYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQQRY SLFLPLHELWKQYIRDLCSG\LPD\I TQPQMIQAKLLK\ADL\HGGLFISVT K\SKWPLLMLGITGNPFYQETK\HIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFPSLGQVNR\SA KKFQSEGNRLTL
2233	7730	A	2428	2	484	PDSSGPHRLRENPPWCLSPADKTNV \KAAWG\KVGAAHVRSMCAEALER MFLSFPTTKTYFPHFDLSHGFCPL RATGKKVD\EALTKRRGAPLDDMP NAL\SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSWVSC

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2234	7731	A	2432	197	332	
2235	7732	A	2433	1	1788	
2236	7733	A	2434	3	111	
2237	7734	A	2435	220	423	HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIKIPYPKKKKK
2238	7735	A	2436	273	499	RSGVRDQPGQHKGKITSLLKIQKLAR RGGACL*SQLLRRLRQENRLNPPGG GGCSEPRSCHCTPAWETEQDSISKIK
2239	7736	A	2437	1	1176	
2240	7737	A	2438	245	394	
2241	7738	A	2439	458	701	GPAPTRRGPAHGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHHPG SRASGTGPGPCQRRRS DHSSAGK WPLREASL
2242	7739	A	2440	365	814	AALRSSSENSRHRSLVKMSDKKAK DPVN\KSGGQGPKRKNWSKGKSSG TSFNN\LVLFDKATYDKLCKEVPNY \NLITPAVGSERL\KIRGSLGQGPFG ELLS\KGFIPNWFSKHRASSYFTPGIT KGGVDAPSLLGEDCMNRSNPPVHLE K
2243	7740	A	2441	41	565	APSPRRPWGHFTEED\KATIK\NLWG KGEMWKDAGGKNPWERLPWLSYP MGPQRFFDQLLANLSLCPIMGNP PKVKGTWPRKVLTSLGSAHKSTW DDLKGHLLPKPEVNLC\DKPAMW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRA SWGRKMGDLELASA LVPSRYH
2244	7741	A	2442	3	284	
2245	7742	A	2443	1	3339	VEGMTCQSCVSSIEGKVRKLQGVV RVKVSLSNQEA VITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGP DIERLQSTNPKRPLSSANQNFNNSET LGHQGS HVVTLQLRIDGMHCKSCV LNIEENIGQLLGVQSIQVSLENKTAQ VKYDPSCTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIAIAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VSESCSTNPLGNHSAGNSMVQTT DGTPTS VQEVAPHTGRLPANHAPD ILAKSPQSTRGSGHRRKCFFTDSKG MTC\ASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEEAVMEDYAGSDGNIETIT GMTCASCVHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKIIES KTSEALAKLMSLQATEATVVTLGE DNLIHREEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADESLITG EAMPVTKKPGSTVIARSINAHGSVLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTVAAQN

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						GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLGDEVATLPLRK VLAVVGTAEEASSEHPLGVAVTKYC KEELGTETLGYCTDFQAVPGCGIGC KVS NVEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLCGMIAIADAVKQEA LAVHTLQSMGVDDVVLITGDNKRKA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKVMAMVGDGVNDSPA AQADMGVAGTGTDAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGPIAAGVFMPIGIVLQ PWMGSAAMAASSVSVLSSLQLKC YKKPDLERYEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSSLTSDKPSRHSAAADDD GDKWSLLNGRDEEQYI
2246	7743	A	2445	14	503	NNDFIVIGTGTEFGIPGPTHAYEKT IYDDYNCL*QEELETENQNLQ\RF YDKRKLEAMLQGMVTETTMKWEK ECERRVAAKQLEMQNLWVKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV
2247	7744	B	2446	226	347	XGKIIVASCFPFSSSRKRRSSTVAPA QPDGAESEWTDVETR*
2248	7745	A	2447	8	2985	WIQYSSTLTPNDWNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/YYCRVRPLGFPDQECCIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVGTSGKTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMITVQEFCKAEVDEDSVYGVF VSYIEIYNNYIYDLLEVPFDPINPNL HNLNCFVKIKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKLVAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLKFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAIC\GLTPRRRYRNQPRGPIGN EPLVTDVVLQSFPLPSCEILDINDE QTLPLRIEAEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSENHNM QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLQQ ELETQNKQLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLVWKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPILRHRRSRASG

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						DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EWDRCR\NKVFCGL WEMR\AGSQLGTWISASRHNPSAKS HETDSPSTERTFSFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFPYGSQKTTSIQ\QNVYSVCFA \SNINSRGRRLRVSSL\YEF\FIMFFLK YISCILIN
2249	7746	A	2448	20	349	SFCLEFPCRPGELLALQDSAQNSTF DKTALPLPCLAPCPPPLGPQS\THIQP CFPHTGPCAPFFTDDLQGGRLSLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP
2250	7747	A	2449	3	384	PFLSVVSSQVAGHGRIFQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKQPADPPSLGT\QCPPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA
2251	7748	A	2450	1	1503	
2252	7749	A	2451	1	855	NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRARFL SQRPAAAAAAQRALMQAIKAG GWKAEAVGKTCLLISYT\TNA\FPGE YIPTVFDN\YSA\NVMVDGK\PV\NL GLWDT\SGQKDYDRVTPPYPPA/Q ADVFLF\CFPFVSPAS\FENVRAKWY PE\VR\HHCNP\TP\IILVGT\KLDLRD DKD/TRIEKLKEKLT\PIPTYQGLA\ MAKEIGAVKYL\ECSALTQRGLKTV FDEAIRA\VLCPVPVKERGRENCLPV VNVSAPSFLGPVPLEPL
2253	7750	A	2452	41	556	APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEKCWKEKTPGKGSLLVYP\ WT\QRFFD\SFGN\LSSAFAHHGQTP KVKAHGK\KVLTFLGRCQSTLDD LKGHLLPKPEVNCTVDKPAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWVT\GV\ASALVP SRYH
2254	7751	A	2453	2	454	RSFFFFCEVGSWVGSMRVVMARL LSEGEQCIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLFL VSLGTDLARGRNSATGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QG WVSTSWGSSSPSVPQFFPKLLEF TGK
2255	7752	A	2454	94	218	
2256	7753	A	2455	266	547	
2257	7754	A	2456	2	494	RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWLVLSSLGIQLAWGFYGNVTGL YHRPGLGGQNGSTPDGSTHFP\WE MAA\NEPLKNPTENKGRQQRVSKGI

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						HWVCWLLHWVLLLPRPQGQPAGG SGLVAGSTQLPTGLGLILPS
2258	7755	C	2457	12	356	MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX X*
2259	7756	A	2458	764	1135	LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFETESCPVAQAGVQWR DLRSLQAPPPG\SRHSPTSASRVART TGAHHYTRLIF\VLVETGFHHVSQ DGLDLQDQFLESFLFCLLVIRLRT
2260	7757	A	2459	1414	1761	SAINFFFLFETESRSV\AQAGVQWH DLRSLQAPPPG\SRHSPAPASRVAGT TGTRHHARLIFFFFFFFFFVETGF HRVSEDDLDLFTSGDLPTLTSQSAGI PGMSHCAWRIDGI
2261	7758	A	2460	63	542	TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPG\ASEPWWQLQSHH PLPPTPQSPEGGEFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCPLR VPQFPHPPLPPSGRKRDRERGMEEGE GGWAAGERRGKEETLGRGPFTQR ERPRNQEGEGG
2262	7759	A	2461	2341	2443	GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL
2263	7760	A	2462	28	403	NTTTCVKGLQTQSYKTSPDGNTTK QTNKVKHTHTII*II*NAPPAVSTTAIR NKFSKNGEQRFIEPYTNRPNHISIKL *RTIQQYASSSKNLEIKDFS WKKLQ* FLENRNKHECFQLFPKVNVGAS
2264	7761	A	2463	727	1156	ETTLSEARRGRSAAASCRGSALRRG RFPESRRGREAPVCPRHVLL*GAQ SKQAAVAGKRSRGRHASRWPKSLF TPRRRRISLKRALHFWQQSADPSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGGERQDWRK
2265	7762	A	2464	10	302	MERFEAGLSHISPWLCPC*CCSHCGD CLLGSRSWGLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFLL
2266	7763	A	2465	303	531	VLRICKVSEENSLFPLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRW E
2267	7764	A	2466	6	100	
2268	7765	A	2467	2998	3570	QDRKQGSSAPATPSRA*AAAAARAP RRPAGRWRG*DAPQSPAEPAPRSP WRRAD
2269	7766	C	2468	125	404	MMARPPPWLESHCTRVVRADGQV XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX ADAW*
2270	7767	A	2469	1348	1807	CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCFLR

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						WSLALLPRLKCKGPSTHCNLRPLPG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVGGQAGLELLTSGDPP ASASQSAGITGVSHRARPSVWFSNQ SMNP
2271	7768	A	2470	538	676	VKRNPEAGAVAHTCNPSTLGGRRGG WIS*AHEFDTSMGNMT*PHLYK
2272	7769	A	2471	40	336	EYLYRHFKNKFLYANILCSSGIWR HYVLILRTVSELLD***GCRWGLSRS FDYLSNTGWV*VLLDISSFAFVTGP LIHGTGGLSAFDLHCEALSFYRD
2273	7770	A	2472	2063	2406	SQKKKIQWYLRMFRQFDIYVCFLFF SVVLLMIGGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF
2274	7771	A	2473	22	273	LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSENIYPLSIKS EIEPIETRCNLNRSNASLVQK*YGHKT GLWWLP
2275	7772	A	2475	1269	1511	INFFFF*IIDRFSLCHPGWTAVAQSR LTATLLPSRFKRFLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA
2276	7773	A	2476	1411	1827	LHTCCLRRRPSGRGRSQGGHCSQSG SSPPRRPRSPAPEGPGFHAP*LCIPDL GHGSRKRGCWPPCGPRTGWADLV ASAQAACGCQGGPPPSGCSL*GRG PVGGSGHGSPCWPLVELCGRCWSW PGVAGSTWQWRRHPH
2277	7774	A	2477	1345	1642	WQQFTGAVIHLAYVVLCLVLAFS SVSLGLNFFHKNFSFDFQRERCWLF SPFKGCC*RCFFTQSLYYCQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP
2278	7775	A	2478	113	584	WQDYIYKEVRVTASEKNEYKGVV LTTDPVSANIVLVNFLEDGSMSTVG IMGHAVQTVETMNEGDHRVREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDAPRTLCAVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ
2279	7776	A	2479	658	785	KTHGWVQWLTPVIPAL*KAETGGW LEPRSSRPATQRDLS
2280	7777	A	2480	2	598	PLGKGKFTGQSAQLTTGTTPRGLILA KGSATLQKHRINHTLTHKNPFLEE FWESPPSLNLALIKGLNGFCLGTEK LFEQMTYGGKVKKCPIGYFALQS WEFHPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST
2281	7778	A	2481	253	286	NDDDP*LPCLGQPPRSCQPSSLP*S LLWSKMTTTPAQRSG
2282	7779	A	2482	407	587	QAGRGRARGVSEEARNKPVPPPTET PQPTLSPQ*MGPAQDPAPQQDYRG KKSLNAWCGRS
2283	7780	A	2486	246	519	FQFGIHNTNYQRQGAkvffknkgv

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						WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFIITGDYSQH
2284	7781	A	2487	470	977	TPPPAGLRQRGYPNRLRNW ARAKGGKTSAGRVTQP*FPEQQLP PGRPWPVPRPGCPHLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDGTG LLASRKLRAAGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSPPSA PAGHSLSHPSRTGKLALVPGH
2285	7782	A	2488	393	618	IREWVNIFWNIHTEEYYTVIKKN*V CQTWWLTTVIPELWEADVGGSLP RSSKLR*AMILPLYTSLDHKARLSL
2286	7783	A	2489	308	626	IRGTSNMNRKNVEKAYYAEA*LSL
2287	7784	A	2490	1222	1374	AQQVKRLEGQRGWKLGRGRWL TPVIPAL*EAEAGGSLEARSSRPW AKK
2288	7785	B	2491	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFIISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
2289	7786	A	2492	1	437	DPRATEGMVVADKTCQKSTGRLE LVTAIRMLKQMLFRYQGYGAAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDS
2290	7787	A	2493	2288	2668	FGRGHYCRRSVSQEEEA\KNLVSEAI AAGIFNDLGSGSNIDLCVISKNKLDL LRPYTVPNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDG\VLSTLSTS SVPKSTSHDRLRLVTCFMTVGCCQ V
2291	7788	A	2494	3	861	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLP\PRPKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFIISPNIYCCGAGTAA DTAMTVTQLISS\NLKLHSL\STGR\LP RV\VTANRMLKQMLFRYQGYGAA LV\GGVDVTGPHLY\SIYPHGSTDK VP\YVTHGFLAPLA\AMAVFEDKFR P\DMEEEEA\KNLVSEDSPPQFP WRIFNGPGLPEANIDLCVISK\NKL GFSPNTQLPNKKGTRLGW\RYRCEK GTTAVLTEKIPLLWST
2292	7789	A	2495	466	607	KKKERSC*LWCPS*SLKNYGLSCR KKKGAVKKIILVQAWLMPVITV LWEAEVGGLEARGLRPTRATW
2293	7790	A	2496	449	694	ILRILGTPISFPVNKISFLPFKCLFDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETIILSELIQEQTKKHKFSLIR GS
2294	7791	A	2497	52	298	YNIEEQQNKRTQSNRHRPTPPPEPP NPEW/TPKPTPTK/PSSPQGE/P TGGPAPHAGAAPP\PSANPTLFPS LTTGGKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2295	7792	A	2498	112	485	YNIEEQQEQTYSKTE*SAQTHPSPGT AESRMEPKPTPPTKRLPPTGGGGRG GTWGDPPGPCWGGHPPVFPSPCPTP TLFPIFDPLGGQSLAQLGWSMVET LQRATTLSTFLKMGKKETVAPPQI
2296	7793	A	2499	32	392	RPTFGIWFYPQVFPELLLELKAKYIG KHCFSIHSLPDTGPLPGCP/SPPGRA ALGIIPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPGQ SYFPAHPPTSSLSLGGIY
2297	7794	A	2500	914	1417	PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFGKFSSLPDTW GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSSTLVWRMLNSASTS PSPAPSYISPPFPGQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPCCAPLL TSPPLTFLKSPRP
2298	7795	A	2501	1120	1159	ERAVCGC*CIFVM
2299	7796	A	2502	1145	1367	IFFSFLHIYIHNTHTHMYIYYTLCVC VCCVYGMVCVACVYSFSSKPKQVC VWIEGNLNY*LQVVCLWYLDPFHS
2300	7797	A	2503	155	454	GGFSVWHTETPPRMRLMHQVQFNL EYLTTPESTQKGGPTPLCIYGYVFFK SDYLYSLSLFFRFLYFSSLL*YMLL VNFLFRMLFSLFMSFCYLFHIL
2301	7798	A	2504	901	969	RWPGMVAHACNPSTLGG*VGDP
2302	7799	A	2505	903	1339	DKTVQSIRSMGGWKMDSKSKFV DLWIAEGIGTSWRNPGYQAPRPFH HGCWGDGKSPPLPKPVSHITDVG WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLQACSEGGAFFSIELFAGRS
2303	7800	A	2506	433	548	PSEYTLGFKNPBKILTFNGGNSMSG VHF*TGFTFLFL
2304	7801	A	2507	637	906	RIKKLSDGSYFLPGVSQIA*GSNYF* SKLGPDDGGASRLQSHHLGRPKVGV FHHVQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL
2305	7802	A	2508	211	575	RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLPGAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPPCSSS/CHGRSHS SPC/CL*SRTSSVVGDEVCNTL
2306	7803	A	2509	274	488	SGDKTMQLRGPCGGWGSCPAGLGT CTAGSP*LCHKKGHCSTHSTCFCLA TVSPCAIFNSTSKAGRGAQP
2307	7804	A	2510	83	442	NFTMVMYTDHILRNAHLMYTSGR RLSVPKIACHITDHSLTHTCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFECLLAGRTFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG
2308	7805	A	2511	2	270	ARLGLPKCFFCVFVKTASRSVSQA GVQRCDHNSLQP*PPGLKRSSLASR VAWTTGSHHHAQLIWLCLFKQYFV SSGFYLLVALWWGG
2309	7806	A	2512	234	409	KGFYAHEKNARTWWLTPIPTLSEA *GGKMA*ARSLRPAWATIRDPISAK

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						SKKKKKKS
2310	7807	A	2513	78	460	NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPRHLQGEGLTSARKRVLR LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ
2311	7808	A	2514	67	279	SHRVSRDAAACGAAPAAARLAGGQR NGRAISGRPGLSS*GAGGGNVFKVC LLLNKNRTGGGRGHGYLSLQR
2312	7809	A	2515	683	933	YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRRGEDAHSWSQRGRQEFV FYLKSTRNW
2313	7810	A	2516	2	208	SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA
2314	7811	A	2517	426	601	PSFRIFTQYSSFLKNSLKR LGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL
2315	7812	A	2518	55	489	HSALIQASVWFRYKYPCGYLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCSGPGPDWLI LGKLGPLGCSKPKGSHFAFLVVPFIF HPCSKTKLFPREELFVVR
2316	7813	A	2519	52	286	MMPCLRQRQREREREREREREH MRTQRKQLK*WITRFKNNSSKRQR TEKNSKKPPVPHRGAGHSNGKLNC FRPAAS
2317	7814	A	2520	3	296	TNTRYTIGDPALQDMNSRRRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHPSLDR*SSGFWDPAGRGE LMQWEMPQPCSPQPLPKPCRSSI
2318	7815	B	2521	83	241	SEWQKKLTPEQFYVTREKGTPEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI*
2319	7816	A	2522	19	629	YFVLISPLLTSTHGFDCYLCINTV HKTPCVFRSLWDIQKEVFSIKGSRSP SPSKGNFGDSEGPVRTIPGGLTVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDSVISSCSIVYVFHSSEKKYCSG TGWPSFSEAHGTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRF CINSVALKFKPRK H
2320	7817	A	2523	1	707	MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGLEAGSLATCELPLAKISE WQKKLTPEQFYVTREKGTPEPPF\SG I\YLNKEAGMYHCVCCDSP\FSSE KK\YCSG\TGWPSFSEAHGTSGSDE\ SHTG\ILRRLDTS\LGSA\RTVVCKA /QCESSILGHVFP\DG\PGNGQRF\CI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIFHNSLE
2321	7818	A	2524	303	743	TGAQWGRGLGHVCWSMGFVSWEE

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						CSGNGLSQAGLVKLKLLIHLHSTVQK GLTPRWGGMLNTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPSSGVSVPQPQCPV KALPVL RAGWATQPPGSFLWPTPS D
2322	7819	A	2525	102	421	VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGA AVAGL*GAAGCRGRSRP LKS RDAGLKS
2323	7820	A	2526	225	448	TQEGRGIDFGPWWPQLLPSSSPSG L*SPATPPQAWVPPLPSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL
2324	7821	A	2527	43	390	GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPPITGQCPLIVSPSYTVLSPHYK VVSPVTR*CPPVTG*CPPIAGQCPPL *CPQAISWSPVVTG
2325	7822	A	2528	525	635	HIQQQLWWPMPVISALWEA*EGGL LDPRSLRPAWAT
2326	7823	A	2529	66	432	TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGF CG WKAGTDFPTSKKPCPLPHNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRLSLGRAE
2327	7824	A	2530	5	95	
2328	7825	A	2531	1	123	
2329	7826	A	2532	118	363	
2330	7827	A	2533	23	250	YLIVVWICISIGLYTY*LIIRALYILR KLTLFKYIPISH*SLSFIVIFCSLVYIY MYIYIYVYIYIYIYIYIYIY
2331	7828	A	2534	346	611	TSVEAQDATDRLWPDSCCPAHGAC TRTVWPKKPPYFPVKKMESCSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFCQ
2332	7829	A	2535	267	682	HFSSLRMQARPPSFRPYLVLPKNC WIFILINDSWMVLFEEASLPTVPSLV QTTIFLLGILQQPLTDLPSTSTPF*S LHLSAV*VVFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKKSR
2333	7830	A	2536	45	280	
2334	7831	A	2537	1560	1885	QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQSRG LPNPKLGKNPLGPISSQKPPCGGPV KTSIVAHNYSALSLSLLPQPGSA PQALSL
2335	7832	A	2538	60	341	VTLSLVILFSAHICRIKLNITINLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYRM*SEIHYIFILS VVLNVNEINSIIQMY
2336	7833	A	2539	442	686	TSYNNLLNNLNKNIETFRKELSSLSHL CNRGQGILKSLIAWLGA AAHAGNP STLGGRGRRIA*AQEFKTS LGNLRP VSPKK
2337	7834	A	2540	459	603	GFLLEIIDKAEGGAHACNPSAFGGQ

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2338	7835	A	2541	1	188	DGRTT*GQEFKTSLSNVTRPHLY PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY
2339	7836	A	2542	582	825	GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWPGMVAHA CNP GTLGG*GRRIT*GQEFKTS LAN MVKLCLY
2340	7837	A	2543	775	1019	DRSSPKKPPDDLPEFTEPQWFTLKH KQCFSDISRLRVGPGMVAHAYGVA YLSTLGG*GRRIT*GQEFETSLANM VKLCLY
2341	7838	A	2544	303	429	AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPTWGSWKT
2342	7839	A	2545	853	867	NP*NLACFCVLEFPSSF*RGFRRLG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY
2343	7840	A	2546	357	560	KGSLVGLSLEERIFVAVQPSLFHK KCLWQGTVAHTSNPSTLGGQGRSV A*PQEFKTS LGNIVRPL
2344	7841	C	2547	486	728	MWVGWVEVFSGVVLGWGVPVML QSDGSWKLVPVHLHELLPFHMSWYP PQDDPNIWSLKQLGLPGCPPLSLC DVS YMVSSA*
2345	7842	C	2548	240	332	MACFSFTSAQLKDRLLRSPATHTPL LNAPL*
2346	7843	A	2549	2	603	SLPYLPQHPLEFGPLNLHRDQ RAG AQTLTQPM SLCCSKSLQLPNALTDK RPCWVLFPA GLSSLLRND SAKLPFR NKSGFP PAQGLCPGGSRLTTWHL SF HGLFLLHQ RSAQRSTS QIPSNHTLT *CPTVTTETVPCLK*PRLSVSVCF C SGSP*RALQCTPPGKPS PFLSQLSLT DPLPSTNLLFHPVGT PRAPGWA
2347	7844	A	2550	132	419	
2348	7845	A	2551	1083	1563	PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPAFSLTSRWDCRRVPPRANFCIFS SDRGFSMLVRLVSN SRPQVIHLSQP PKVLGLQVETGPQKREWVPRELTA SGQWK GQEPDQGEDSGTEGRWLPL LPSAGHSGED
2349	7846	C	2552	173	501	MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSPTLSRPLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGV SXXRP*
2350	7847	A	2553	174	364	YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE IS LANMVKLHLY
2351	7848	A	2554	61	283	GGRIA*TQHSILDNRVRLHLK KKKK KKQY LKKVHLPGAVAH/TYNPSTL GGQGGWIT*GQEFETSLANMAKLC LY
2352	7849	A	2555	1140	1313	HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETSLA NMAKPHLY

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2353	7850	A	2556	99	296	WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYN
2354	7851	A	2557	175	332	RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY
2355	7852	A	2558	667	772	ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY
2356	7853	A	2559	7155	7302	IMKLKMYIWP GAVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY
2357	7854	A	2560	227	410	FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTAVR*CSLFQGSYGIFGI EGRIPYSEL
2358	7855	A	2561	275	685	LKPLFTPSPGPAGVPRGLCWKEAPT PGSLLGEEETELNVY*GPPGSLRPA SHWAPPEGLRPTSPLFVAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL
2359	7856	A	2562	20	354	PLYSQSFPIIYPFITLLPE*SF*NNNYC SfVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLTVYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS
2360	7857	A	2563	374	585	GNLINC*LHTHTHTHTHTHTHTHTH NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAIRNA
2361	7858	A	2565	918	1096	HCHSNSEFDTETLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR
2362	7859	A	2566	101	327	LVKNQQSTQKLAKHGWACL*SQLL ERLREENHLNAGGGGCSELR*RPCT PAWATETVDSLPMCLVLQPFLSL R
2363	7860	A	2567	347	478	RDHCRLGTVAHAYNPSILGGQGRR A*DQQLETSIGNTVRPLY
2364	7861	A	2568	622	761	KSVEVFYLSIGQEECLPHIQFIFHAT IFIIGRAQWLTPGIPAFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A
2365	7862	A	2569	70	316	ISHPSPSTRWEAVTWALG*LFPCPC HLQGGRQAPLPLPYPLPIVVAPPLI SRLNPDGDL SAKTILDVTLYISSTTV GGSWG
2366	7863	A	2571	145	331	IFHSKMPISEWKLV*TLWQFFKELKI ELPFDPAIPLLGI*PKFQRLKNTNGIC HYFYM
2367	7864	A	2572	918	1135	GFISASLCNWILTHLKFFKEMGSR VAQAGVQWLLTGAVMAHCNKLKLL GSSNPLASAH*VAGAICMYDHWHA
2368	7865	A	2573	590	936	QLAACGGSCLSQHFERPR*EDCLN PGVQDQPEQNRETPISKILKSWA WWHIPVVPGTWRADVGGLPEPSRP KATVSCDCATALQPGRRRARLCLK NKYIKYSVQKCVIFFLF
2369	7866	C	2574	34	670	MXVFLSSAGNMPVTCWCWEAPRC

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						NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQPRVVQTDAAAXMVE VSVXVVLEGWGXPTTRRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRVGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLAGRRXSGSNLI*
2370	7867	B	2575	70	165	EQIEALLESSLRQAQQNMDPKAAEE QEEKEE*
2371	7868	A	2576	1	390	FFFFFFGVLPVLFDFHVCFLVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LVFEPDVS WLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPAGFSRPLYPCLGPPN
2372	7869	A	2577	435	861	RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPPEHGSRLPQPS/CAAASV*TTR GP*GTLCLS*WGKGTSPGCCGIERP KAGGKCTGHSGVCPVTRKSNHSLC ARSPTSCRPKFAPAAAGPRGGALPG RVILCSKAISGTGPPRPTPPEHGSRLP QPSWLRRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCPVTRKSEGLGGGRLGLCISGCT AALPSTNM
2373	7870	A	2578	38	398	PVLFLDFHVWLVFVCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNKQA ESMSLCGFFLPDCFFLT YKRIYL
2374	7871	C	2579	42	443	MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCGRVILCSEAXSGTG PRPTPPEHGSRLPQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCIE RPKAGGKCTGHSGVCPVTRKSEGL PAEDKKTNMKV*
2375	7872	A	2580	871	1253	PRLPPGLPGADRSPAGSQACA\GPA EHGPQGRGGGGGGGGGGPGLPHP PTCGTWTSEGA\SRRAPPPAAKGG AGPRCSPDSPSSPEHFD TQKGKLHS PCCWLFFPLLFPSPISDLSKRKRLPK NCL
2376	7873	A	2581	222	754	YPP*HVAPHPAPLPWQVQGPDPW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPFSLPNLSDLGTS FPLPQTLPLCPAPQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHTLLV PTFSQSSQNPPLPSPSPIGAVKALFAS TMG
2377	7874	A	2582	2	431	PEGAAPAAMAVTALAARTWLG VW GVRTMQA\RGFGSDQS\ENV D\RG G\SIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSRQLAALKKHHEEEI\VHHK \KEIERLQKRNL SRHK\QKDSKLLKH

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2378	7875	A	2583	1	232	RETACCGRDARGAAPAAAMAVTAL AARTWLGWGVVMTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR
2379	7876	A	2584	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGVRV/WGVRTMQA \RGFGSDQSENFPTGPRAPHP/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEI\VHHKKEI\ERLAEKK FERHKQK\KMLKH
2380	7877	A	2585	3	316	LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLDANHDG RISFDEYWTLIGGITGPIAKLIHEQEQ QSSS
2381	7878	A	2586	3	469	
2382	7879	A	2587	434	815	TQVDWTQRRARPGWRHPHPFPDD DSLGCCTSHLPPHGD*L*NPSSNGA NPRLSPAPHPPREAQTPPGAGHR TPLSRACGLAFAQPVRLRRDTRK DGRKEQRETVPPTPPFDARGTRLIL RHK
2383	7880	C	2588	204	354	MWLQMTRAVLSSNLDPYVCRRRA RGRSSPSGSLXXXGEESWGPRHCY SP*
2384	7881	A	2589	390	681	RERGRRAGRRETAVRSREKERER EGLDRSSRKR*PELVKGSRAH*PQ SGRWSHRPRPAIVPTSFQPCDVRAG QPNGPSDLPDHLPTRRRKACDRR
2385	7882	A	2590	598	769	YPOCPTPCQAARVWWDHSLAIPAL LGGRGRWII*GQEFETSLANMAKPH FYQKKKKK
2386	7883	A	2591	359	775	KKTQPLHQGYPKINFRSPSPPIVPV PLLALPK*GHSPFVSPPLQKIPPKG SPHDPTRQRPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRFTSKRGKDGIPFDAQG LQGHKGTFFFF
2387	7884	A	2592	585	780	TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRIT*VQEF ETSLANMVKHLY
2388	7885	A	2593	436	1645	GMSALVQSRVSHLHRVSLTRLTA RAQETSSPPNTVTPNQTLSTAQNK RTIPGPARE*VTLTRLKEPLLVEK AAPTTPHQ*GPAPRLQASALPLYPE QHRRAPSSSEDWPRLTPPSH*GVS TWTP
2389	7886	A	2594	1	373	TCSCPWLAPLTLQKNCPPHCHILSL LRKTKQNDAPKKSPPRSLPAVSGM KQDVTTLGRMEKPPRSIPQRPQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS
2390	7887	A	2595	502	798	SPKVQRHSSQAALRQAGGALSLLWG CLPSQRRPRTVSSREGPHPGKGV* GGVQRSKGPPLPTCPQGLTCLTPT DPGSAWNPTPT*NEKGNSEIRH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2391	7888	A	2596	1	136	HPCVHEPMSFEWPWQYRFPFFFT*G SDPKKHGWASLPSPGPWAQP
2392	7889	A	2597	429	1003	VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFLSLYSIIPSDVLPSSPFE TRVSWEQFAYLLLESAYLLVQAIE *ASSFFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIIFFRGSHCSLQYDPGFL TLNAPSITI
2393	7890	A	2598	367	463	SGHGAHAYNPNTLGGRRRIA*SQE FNTRLDN
2394	7891	A	2599	436	833	CLTSALLGCYVYFFSPHPALFFLRI RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMLCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLFVHLLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY
2395	7892	A	2600	53	95	DSILLLTQAGMQWCELGSLQP*TRP PIVCFCLFIYLLRQHLAPHSWNAV V
2396	7893	A	2601	432	825	NFKDTAKGFLHFDHQQKILDPCPLG SRARFGTYPECPHVPSTEAQETGL SVPSFGFHFHFLTYFLLLEYFYH*G TLYLHLDLHOK*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF
2397	7894	A	2602	83	111	
2398	7895	A	2603	1	71	
2399	7896	A	2604	215	758	LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSSPRLGLQ GSISSASRGRPAQHVPGRPATLSPP AGAGPSR*ERSRAGARGRWVLLDH AGERPAVRELSRPDPQVVSFGPRNIS EIGQVLSPETSSCELPGIGDLLLWQL EYVDARKHSLVGPESLSHRELGSPA GGRP
2400	7897	A	2605	211	323	LDSLQHSASTLAQHSASKPWKPD FHTQFFHTVWKLQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNVCWKLSGFHGFE AECCASVEAEC
2401	7898	A	2606	75	232	TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFPLIW F
2402	7899	A	2607	325	566	FNDKYFYYPRGQIQCHITLFLNLKI TSDDFFCFKKTG*VAHTCNPSTLGD *GGGIA*AQEFKTSFGT**DPIYKN
2403	7900	A	2608	1114	1367	AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNNNS*RYTKCIRKFNNLSEPF NHVCKVF
2404	7901	A	2609	100	450	FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYK*V GNFDILYHTCVCVCVCVCVCVCVF VCLWSTLRMTDTV

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2405	7902	B	2610	50	382	XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESL DSESYLS EEGQELSD EDEDEVYQVT VYQAGES DTDSFEEDPEIS LADYWKCTSCNEM NPPLPSHCNRCWAHX*
2406	7903	A	2611	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2407	7904	A	2612	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2408	7905	A	2613	1	752	DL DAGVSEHSGDWLDQDSVSDQFS VEFEVESL DSESYSPSEGGQELSDE DDEVYQVT VYQAGESDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGKDKGEISEK AKLENSTQAE EGFDPDCKKTIVND SRESCVEENDDKITQASQSQESDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVSSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE
2409	7906	A	2614	426	813	SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRHRLGYAGT AGPLAGYRPFQRHRSQSLWRAASAI CVD AISMRTRSRSSTVRPLWPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL
2410	7907	A	2615	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2411	7908	A	2616	1174	1354	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT
2412	7909	A	2617	2271	2393	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2413	7910	A	2618	1029	1197	FFFFFFFFGFLVETGFHRVSQDSDL LLTS*SSRLGLPKCWDYRHEPPRPA EEGI
2414	7911	A	2619	402	990	
2415	7912	A	2620	1326	1716	KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLKAGCSGSCL*SQHFGRLRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH
2416	7913	A	2621	148	420	LSLSLCRFLGRFCSSGSSSIFVLFHF SFL*FMFSFSLETQKFKHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFILSEKWR
2417	7914	A	2622	565	916	VPRARTQHSREKGRAGAWFGLHY QGSII CGSNSTW*NPPQRGPKLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT
2418	7915	A	2623	1132	1245	KWHLGKIQNYSTGKCNRIYIYI*I YLF*CHLSIGNC
2419	7916	A	2624	209	326	
2420	7917	A	2625	808	1010	EETEGRARWLTPVNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK

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						KKKRKKEIKPGMVATCL
2421	7918	A	2626	1602	1940	PSGNTSETSKGLNIRSHTRLFEDIKG VNHRSSQLFQKKPKNRDRIFQERYV RSLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK
2422	7919	A	2627	2565	2748	KSLKLGMSLKIKFIFLIKGH LGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY
2423	7920	A	2628	1032	1292	MYIPLNNGTVGVDSQMHLDVQIDY RVLFSDYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL
2424	7921	A	2629	1640	1815	NSKGESSAPLFLPD SHLEKRKSYGT HPLYISLLKNYEK*NNSNLKAVIFK ALLKNKQT
2425	7922	A	2630	1089	1226	IQIQNKLLKECPSWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT
2426	7923	A	2631	197	430	SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCLRFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRTTAL
2427	7924	A	2632	343	596	GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DNGKQM PCYYRAASEG
2428	7925	A	2633	1143	1553	QCRRVPRGKRLELGVHSSSTG*QAPL LPSASATSSGFLADRRVGTGLRTPL RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAASAAISARSSPPSAAGS GPDWRRPGKRHSRPTAAASAHTS PSQSPAIPAGGR
2429	7926	A	2634	158	585	ALTWVHLSSVSFFFDPDLKLTSPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLLVPKAKLW SHVGRMEGDLQCPLCLWLHLPILW FFGGSCFPQTEHSPVQSPDGLIIAWN CPASDAGIKDCLPKYFC
2430	7927	A	2635	1348	1540	SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTYIHVHLMGYVKIKQ LFNACDSMEHLQAH
2431	7928	A	2636	263	615	LVNSEGNIWVKLCHELQHGPLN SSP FLILLSHSEKINRASIMLRKYKLIN NYILSAFNPPPGKIHTHTHIHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE
2432	7929	A	2637	270	665	KLGKVAHVYPYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KTQTYPGS GF*PSHPSCCKSGPKPLMGCTPGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK
2433	7930	A	2638	54	311	SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQKLAGHGATHL*SLL GRLRQENHLNLGGRCSEPEIVPLH FSLGKQSEALS
2434	7931	A	2639	26	229	CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPSPWPASPPECCRDH

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						ICPHPVGPPGPPSLALPAW
2435	7932	A	2640	133	586	THVMLCAQVGSHHPALPWASPEEC CRDHICPHPVGPPGPPSLALPAWDT HTHTHTHTHTHARTRATHAHILPS HAVFYFDFVQSGSLAGSPYPRGGG GGWFLGGAKKGRECPGG*MGGPP MTPSSFQKQLLLPPSQGPTPKPPEGG PCLQ
2436	7933	A	2641	186	609	RVGHHPPSVRHPHQGHGWL RDPV QLHLWSSCVAFPFGGAPAGLPPSDQ DPGPPLAISPTHWPPCGQPCKTIAA HGNGHTRTGGR*RPRL*SRPAEWP SAPKGRSGGLPGSFQEPADSYPGCG TWCSSACKGRQPSYS
2437	7934	A	2642	989	1790	NYTPFLPCSASAEFCELWGRPLVV FCYFYFQPPLAVEP FNIVICCWVR VKVGPGAFPRGLRRDVQRADFSRS SEGLLMGWVRDFDNHQSTCALDPF SGGIGSLLVPGGSDLQIGCFQKSFQA LIEN*CLNRHNSLG*TPKRSIKILWA E*ISRAGLCNSSPEHPACGHPPR*G QWEAGPTAARTCFSPPTSNPPNSG PQAHEAQVSGDHSIGGS*GSPSPPL AYNLSTRKAQPKCGKKCMVLPSTC KNCTYCKPFALWNCMP
2438	7935	A	2643	92	330	RQVCLPPSERNVASLRTPHPRGAQ KSQEGPPGRQSPSELKSRYWCVENS TWVSRAPQGTGWPGWALPFPHQG* GWLGP
2439	7936	A	2644	1137	1290	HGQINQMEVNLPM DRKV*THHTH THHTHTHTHSSTSCPYTLKRNVK S
2440	7937	A	2645	96	357	
2441	7938	A	2646	2648	2953	DWGYLPFKTLTYPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHL YQNISPQYLCQKTPQTKMPLKKG VFFPFRM*APQESGTNVFCMFLCPS TL
2442	7939	A	2647	201	377	QTVFVKLCVYTHIYN*VYMLIHI*A PLSVY*YAYI*AHILSYIYVHLVIYI TEKYDF
2443	7940	A	2648	1917	2056	QSHAKEWIFLLTCFIF*KLLRNIIYI YIYTHTHAYIYIYIYIYFQ
2444	7941	A	2649	246	717	KRQSEEGVFSCCQGWNESLLLKSK VLEYP*FLHFPSFSFDLYLFNYVFIY LFIYFCISQSQTSKAERAYIYIYLY MCCRQNTVNFTTTTQKLFCHLNH LRRRNEKRWGCHFLVYAFEARSMF IYFFSLCINENDPEWRLAERSMYWS KHHKSC
2445	7942	A	2650	191	657	SGGERRNSSAPSAMSPSGSATTSPG T*PRIIDSERTPAFHARASTVKPPAGI NTREHPPLPCTPKPCTKTHFTAPP PQRCTHTSSPPRNLIQIFTRDTHPPPT HTRHTHTQEPGWWSFDWVGCLR GFSFECTHFHFPQNKGTFFKMSYIA TY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2446	7943	A	2651	1108	1282	PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKNKKTETL LRRPVFGAAN
2447	7944	A	2652	2	479	FIIAHPDVTVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLYNIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF
2448	7945	A	2653	341	622	YQNRLFPNQCFTCLLVWLWDSPAP PPRPWQPPPQGF AHT*DRKEEGDPI GIWAPEGKSCPTKPPPPSLPRTSPGW KRALQKGDTCGPGPSTAST
2449	7946	A	2654	597	785	NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQEF EAS LGNIVRPCLYI
2450	7947	A	2655	237	656	RGQGWVGDSSQGRGGAKEGLLP SH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS VLP PPGDRVMEGGPPTPLQHRSPH PGGERHGF S*SKFPPPPGSRPQKERR KGQRGM CVRVGQIN
2451	7948	A	2656	109	290	NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY
2452	7949	A	2657	122	359	
2453	7950	C	2658	133	315	MQWLYIATLIPFFWTQRKGTFS GK SQLILDFLQ GALAILSPDPHPGILHR SLWAHLPA*
2454	7951	A	2659	1399	1644	CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPPSGCLGPFT LDGCGLSPPLYLPVFFPGGLLKSSR PLSCLN
2455	7952	A	2660	592	943	RTGCGQTLTVSHPDQARHWPGPGF ALILLYYPAQGFHLLPEAGPEGRG SLLTEEGSREANSRSSLISAAQLPPA APPQGLGV*MQESSRWGGKGRSKG SLPINLGLNSKLKKTTPP
2456	7953	A	2661	181	401	
2457	7954	A	2662	1163	1457	HPRICWHHSDLHTITKTSHST*SESQ NPHSESPGPRGCEPPGPRGSEPPSLL *LSLPPPLPFAFCSSCPGLMAGFPPK QALSITGPFSPSVALWLGHC
2458	7955	C	2663	275	327	MPFRLSQDCHHSAGAAQ*
2459	7956	A	2664	70	191	DLLQKPQV*DPSRTECVSM*CFLSPP *AETTSILPCFPRI
2460	7957	A	2665	40	142	THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQHPKVLQLQAGSTVNQPA HRC
2461	7958	A	2666	479	722	YCHIFLG GFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC
2462	7959	A	2667	265	518	VKTVFLSGLDPLSLNENNMVLIMTS IVIFSHPLHFRFETLIGEWPFNLILG QV*WLTPLIPGLWEAKVGG SLEPRS

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						LRTAWET
2463	7960	A	2668	626	695	GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTIVIPVLR AEAGGSLEPRGSIPG WATRVPRLYIEKKKKK
2464	7961	A	2669	66	610	TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLLEDLILGELQVLA FGALSGSISIFPSIPPHSAIHKNSHLR KIPPVPPRQPFRRVWTSGPPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPVRSQPE *TPCKKNFLMEKISYDFHSQRSSD
2465	7962	A	2670	1077	1598	YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEV RVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIPAGRDGPGRPGL LAEYRRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVSPWIPGGCRGPITTVGTS
2466	7963	C	2671	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLH*
2467	7964	A	2672	1818	2154	PTPVFVPSLFP SHKHLPQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRDL VSKIIFKKEQK
2468	7965	A	2673	137	1610	EENIKSYKEYKCHNLYVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL
2469	7966	A	2674	1	490	GNRSRARRLASSPGSAAAAAYRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRA LAEQPQGHPTPDL STGDQYCGDYELLSWRLWKQNNNA AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF
2470	7967	A	2677	2	215	
2471	7968	B	2678	63	203	SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG*
2472	7969	A	2679	433	895	VFHLPSAEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTKAR\DNAC\ND\MGKMLQF\ VLP\ VATPRSQQEVIK\AYGFQLPTG EGVP*SFAPIWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLPTPWGLLVG GSVAAS
2473	7970	A	2680	235	442	RPTFFYIPFKISKIKPSKIST*RPPSL VG*KSKEKASTQKCLTKIPVPSANL KDFLPKHDTEKRELH
2474	7971	A	2681	199	1061	RRSEPKGWNRA TAFPPKVGCGCVW EKTGMGDQNPEETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TSTTRAPCENQRGGKQ RSGWLRA TKPHTAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSGK**VMER*WSGKHSVKI

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						VSTFPPSPRGSSSRLKPEARVARKY GPSPQLKPRR WRERKHGKPREMGR SEKSESLEWDRSLPVLRMVDGFSPG KQNRNGQRGRAQSMASW
2475	7972	A	2682	415	575	ISGWGVGGSCSLSQHFGTRTRQEDHL NLGVRDQPGQHSENKVSIIKKKRN VISI
2476	7973	A	2683	457	549	VSTGNKVVPVGQKVKAICI**KVLLK MQIAFTFCPGTTLLPVD*TKVTHL NECNILASLWVLKHDLVFQLLATW LHFNLRSSISENASAPSYCPTGEGVAT LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*ADVSSFQNILQ FIVNHKIKLPT
2477	7974	A	2684	291	364	RLKL*SPHLRSYFEKSKEQLASRTP TGQS
2478	7975	A	2685	2	361	TETLARPPSPLVTNMKLLAETVLLL TICSLEGALVRRQAKEPCVESLVSQ YFQTVTDYGKDLMEKVKSPQLQAE AKSYFEKSKEQLTPLIQEGLGTGT WFNFFELFSVGTGLTTAWPPS
2479	7976	A	2686	425	678	LLGAISWELWGTQCPHPVEGVPGPF GLSNPQAGAFREQPTGPVP*SSSF SKEQLTPLIKKAGTELVNFLSYFVEL GTQPATQ
2480	7977	A	2687	64	287	RQMAILLKANKDLISAGLKEFSVLL NQVFNDPLVSEEDMATVVEHSMN *YMSYYSLQATGEPQDLRPPCCS L
2481	7978	A	2688	983	1386	QEVRYRKVETLRCLLFSSCLVPVCA ASPVSRPGCRFLRSSLHWPTGRLVF RQRGETFLVPEKTVLRGVASAPAQ KAAGRTPVPGRPDARLRADARS*S C*RAARPRRGASGAVGARCGRPG FPFLRSGGIFV
2482	7979	A	2689	473	706	NLTLASKISLKYCKQYLWILFRKRL WPGVVAHVCPNPTLGGRRGGQTT*T QEFETILGNMVKPISTKYQKKKKK RAAA
2483	7980	A	2690	1400	1600	VGGGSGRSSKFPPLP*CPPPSCCSLPI SSPPCLSTPGPSLLHVS KGTRRISRL LDKRISKRFTNH
2484	7981	A	2691	6133	7646	YMLFLFLSTKGWTVIQNRQDGSVD FGRKWDYKQGGFNVATNTDGKN YCGLPGNEQACKIKSFYKWDFF*L KNIHCWKPVLS*EEFPDKNVEAK DKGRKAVFSFPKFYFW*EILFCFSFR VEYWLGNDKISQLTRMGPTLLIEM EDWKGDVKVKAHYGGFTVQNEANK YQISVN\KYRGTAGNALMDGAS\H LMG\ENRDHDPFHNGHGSFQPPYD\ RD\NDGWYVWHSLLL*KSH*YHY SESLTIFLIATTSWALTVSHCPKLFM HHSKAFQL*GRHSYSHFTDEI*RDY VICPM SHNYPEIKLEFEHSYFLNNEH LDKYL YLYILKCV*KLSFSFPGFS SDT

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						KGCKSYYSIIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPK GK TTVHTSVAVFYG*SAKRNLTTVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTDDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ
2485	7982	A	2692	711	865	VTMKTFSLRHKACGQVKNTLTI*Q PN\SSIQPTSHYYPHCQPNTGMLIRK G
2486	7983	A	2693	26	351	ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLCQYFQTVT DYGKDLMEKDMSPQLQAEAKSYFE NSKEQLTPLITKAVT*LGNFLSYFV* LGIQPASQ
2487	7984	C	2694	10	123	MSTDRHQGQRRWLGRPPHCYQHE AARSNCATPHHLQP*
2488	7985	A	2695	6	409	FCPALSSSTALFFLRGLWFRGKRLG STDLT LHKPFNLTPQQLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVVFPPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG
2489	7986	A	2696	736	927	SVAHSSCVSHTHMHTLLGRRATINC LFRNGRGQVQWLTSAPALRKADV GG*LEPRSSRPAT
2490	7987	A	2697	2	251	FFLKPCQLTVATSGGCNFWPQAI FL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV
2491	7988	A	2698	1278	1515	SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY
2492	7989	A	2699	139	260	
2493	7990	A	2700	268	388	
2494	7991	A	2701	233	400	HFLRAKVSVTQARVQWLDNGSLQP PTSM LK*SSYLSL SKCWDYRHVPM APRHFNK
2495	7992	A	2702	602	758	IICLSVI*NPRYTLGTVAHTCNPSTFG G*GTWNS*GQKFETSLTNMAKL CF Y
2496	7993	A	2703	379	1160	LVDMQLWPPVFHENKCLGPPPPQT TH*RPAPAVPTPQAGPGTQGLATAS SVSMLCSDKLPSSDQPRV*PGDAE LSVLGVGRSSRKESPDDQAPPLPVIC ELSFARVGGAPGEPLQRPVVL S*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRPGPENS GS VTAQGQPL GRP*NRTHLFFVPHPGQAASQSQS SSSPP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGGDLPQPFQPV LLAALVHI
2497	7994	A	2704	178	412	LLHSSLGHVARLPTLQNMKTLARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGIPVCS FKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2498	7995	A	2705	67	398	ISLTLGRHHGKINVYFLYLKMQG*Y FCCTFVSVVNCSDCLSGHSRRKTEG DKVRKEKQEA*A WCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD
2499	7996	A	2706	264	612	KHFSYNFFSFSFFLEGGGRVLLCP WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRPKILGFQASA TALGPLTPFCLIV
2500	7997	A	2707	179	472	
2501	7998	A	2708	498	849	GSLLSRAPIPYPLNWVSFFIPEVRTPP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG
2502	7999	A	2709	768	1073	GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR
2503	8000	A	2710	5451	5678	
2504	8001	A	2711	396	687	TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPAPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPAKM WDFWSETFRKVKEKLTDS
2505	8002	A	2712	1	93	LPKRWNSCHEPLVPLFSPLLVNAV GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSPL LVNAVGLGVLGSK
2506	8003	A	2713	376	469	NQLPGPERWLTPIPTLWEARA*GL FEPRSL
2507	8004	A	2714	715	1050	
2508	8005	A	2715	404	559	VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTS LANMMEPHL Y
2509	8006	A	2716	3	180	FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIIFYFL
2510	8007	A	2717	1825	1958	LWTISVFWKAGVPLPC*QSPRWTKS ECLSF TPMFLNKS NFKKRI
2511	8008	C	2718	23	349	MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISGAGL ASKKNAV FQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE*
2512	8009	A	2719	41	298	ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRPP*ILQRHSRQNE GHRQEWCGHTA
2513	8010	A	2720	277	651	KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRLIN EPSNDWDIYYWGHR*TSPRNIWK MKSWALLERLCLKTKTKRQRLRGP SFWSTSLEKPRWSCAPRPGHGGSVC GW

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2514	8011	A	2721	76	185	VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFPQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSDSSR
2515	8012	A	2722	1685	2124	
2516	8013	C	2723	299	577	MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLTVP YRWHTLSGVALFPGPCCGIFFCHSG FQCGRLPYRVHAPQG*
2517	8014	A	2724	14	213	VDMGSHRVSQDGLELMTP*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLSYFCS
2518	8015	A	2725	1169	1404	SFLYFNGLMNFRRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQGQGI P*AQVFETSLDHTPRPCIYPPKKKKK K
2519	8016	A	2726	44	417	CGCGLGEICLSHGVAQHNRSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNLI*WNPGGPGARGFPGL TPPRGGKKGRAQPPENLVF*EKTG FPIVQRGGLKPPPGPPKGGE*RGGPP
2520	8017	A	2727	624	1023	CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFPFGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTINLGFSSSRVPP VTGGGYKPPRPPKGGKGTGGTGT HHRAL
2521	8018	A	2728	36	211	KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP
2522	8019	A	2729	640	898	VLLTCLVCLVSSKTKPNITKQHTKI KFPQSSRARWLTPVIPKFWEA*AGG SPEVRSLRPAAGLEFLVSHLGPCKC WDYRHKPPCLA
2523	8020	A	2730	707	1164	SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICAYNG*RFYLCGMK*GL *SWF*CFSLPSLFTA VKFIKCFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSIKLPSCP NVQ FVSVCVCVCVCVNLIK SARLPI
2524	8021	C	2731	270	371	MQNLQCFRAFELLTHNSASELPLSA PVTYTEDD*
2525	8022	A	2732	2553	2764	GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFORPYSYEQSFPPF* TPNPPIKTSFPPRNCNSP
2526	8023	C	2733	25	288	MSKVQTWGRQKTSHTRLSLHTWK VAQRPRGRGAPHLPDGVAARQRCSS LSTRVCCHHVSPQPNLGAASVG DHSQLACSHGPLQSPS*
2527	8024	A	2734	1043	1207	NMMTTHTLKKVGTGGRARWAHTC NASTLGG*GWIT*QGEFETSLAN MVKLHLY
2528	8025	A	2735	74	233	MVTFNCFNLH*TVTKGFTRLIV
2529	8026	A	2736	11	151	ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE
2530	8027	A	2737	214	369	QKDSPD*SCDCVLKENEISNLRCPIQ

MISSING AT THE TIME OF PUBLICATION

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2554	8051	A	2767	108	279	
2555	8052	A	2768	3	314	LLALVKEGPVPLFLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL
2556	8053	A	2769	1	465	
2557	8054	A	2770	192	400	
2558	8055	A	2771	1414	1597	SGVYKRCKGGGRFVFLECATSGLSL ISS\GLSWG/RLWGHGGCRLAGGWG GGGGGSGGGMALL
2559	8056	A	2772	673	988	
2560	8057	A	2773	749	1169	
2561	8058	A	2774	2	290	
2562	8059	A	2775	3	520	HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YSDKYFEEH YEYRFVMLP\RELSKQVPKTHLMSE EEWRR\LG VQK/SLGWVHYMIHE P\EPHILLFR\RPLPKSSTKMKFISGIV KSCFKFN VYVYKVVFQWNTWRN GYKS FHPYLCMSCILHSNRARVKC NCK
2563	8060	A	2776	1134	1312	
2564	8061	C	2777	49	282	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRPDPTXESQDRLR CAPCTXHQPLPLDTHNRTL VHNRL NIPQKL*
2565	8062	A	2778	1	306	
2566	8063	C	2779	54	212	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAPMPVQSDDSGK RQTG*
2567	8064	A	2780	34	308	
2568	8065	A	2781	35	407	
2569	8066	A	2782	41	360	
2570	8067	C	2783	105	302	MXNLKRLQISMKPAHSGVCPVTRX SEGLGGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV*
2571	8068	A	2784	3007	3541	KRV DYWGIKSSIICSTLLPHRSGLC KYYFFFLSLSFKDSFWIFFFCLSQR WKGERAKEKTTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPAWRLRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKRVRR
2572	8069	A	2785	272	801	
2573	8070	A	2786	659	842	
2574	8071	A	2787	156	203	
2575	8072	A	2788	441	785	
2576	8073	A	2789	2	28	
2577	8074	A	2790	5	1049	LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARRSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGK KKKY RGKAVGPASILKEVEDKESEGEED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EDEDLSKYKLDEDEDEDDADLSKY NLDASEEEDSNKKKSNRRSRSKSR SHSRSSSRSSSPSSSRSRSRSSSS SSQSRSSSRERSRSGSKSRSSSR VTGALLPHEKDLIQVHLLLRGTERE VVLDDLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKFTS
2578	8075	A	2791	971	1106	
2579	8076	C	2792	291	444	MGCFFPNSWVRAGVLIPVPVICLSV RLTWGREAQRGWVCRCSQNWVIFAP*
2580	8077	A	2793	1	672	
2581	8078	A	2794	1	691	MDFLLSWVHWSLALLLYLHAKW SQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLVDFQYEPDEIEYIF KPSCVPLMRCGGCCNDEGLECVPT EESNITMQIMRIKPHQGGHIGEMSFL QHNKCECRPKKDRARQENGSAQAQ KRDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSSRT SASRSREASRPWWATTSWARSR AAAARTCC
2582	8079	A	2795	312	394	
2583	8080	A	2796	490	2890	PVALTDRQTDTPSPSYHLLPGRRR TVDAAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLLGCSRFGGAVVR AGEAEPGAARSASSGREEPQPEG EEEEKEEERGPQWRLGARKPGSW TGEAAVCADSAPAAPQALARAS GRGGRVARRGAEESGPPHPSRRGS ASRAGPGRASETMNFLSWVHWSL ALLLYLHAKWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DIFQYEPDEIEYIFKPSCVPLMRCGG CCNDEGLEC/VVPTEESNIPMQIMRI KPHQGGHIGEMSFLQPNKCECRPK KDRARQEKKSVRGKKGQKRKRK KSRYKSWVPCGPCSERRKHLFVQ DPQTCKCCKNTDSRCKARQLELN ERTCRCDGSALAQKRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLGTFTVTRSKSA GLVVGDNIVGKIKGRGGKNLLMS HMDTVYLKILAKAPFRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKGSFGSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRTMNIDDKAKN LRFQWTIAKAGQVSNIIPASATLNA DVR YARNEDFDAAMKTLERAQQ KKLPEADV KIVIVTRGRPAFNAGEG GKKLVDKAVAYYKEAGGTLGVEE RTGGGTDAAYAAALSGKPVIESLGLP GFGYHSDKA EYVDISAIPRLYMAA RLIMDLGAGKEFH HHHHHAS
2584	8081	A	2797	326	1280	

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2585	8082	A	2798	356	518	
2586	8083	A	2799	27	225	
2587	8084	A	2800	470	754	
2588	8085	A	2801	707	907	
2589	8086	A	2802	2	502	VLSPEEDKATITSLWAKVNVEINAG RKKPLGKAPLVVLPPWTPRGFLWN SFGKTLS/ASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDA\IKAPLDDSP RATFCPSLSEL\HCDKL\HVDPENFK A/LLGNVLVTVLA\IHFGKEFTPEV\Q ASWQKMVTGVA\SALA\SRYH
2590	8087	A	2803	921	1146	
2591	8088	A	2804	1170	1482	
2592	8089	A	2805	1492	1853	
2593	8090	A	2806	909	1180	
2594	8091	A	2807	105	248	CTCSRVSHPNAPRNSLVSMVFRMHH PPPLDTFRQ/PQPSFNL*YP*PNYP
2595	8092	A	2808	662	843	
2596	8093	A	2809	263	408	
2597	8094	A	2810	701	950	
2598	8095	A	2812	1426	1525	
2599	8096	A	2813	1	1416	
2600	8097	A	2814	108	520	
2601	8098	A	2815	3	201	GRGLRSPDVTVTQRRRGRSPSAAER *PTRPGVLRALPAPA*GKHCPWPRP GARRRPPSSPAARPCP
2602	8099	A	2816	318	428	
2603	8100	A	2817	448	647	
2604	8101	A	2818	42	191	
2605	8102	A	2819	3	452	
2606	8103	A	2820	25	519	EFHRLRENPPMVAVSCPTKTNVKA\ AWG\KVGAAHVRSMCAEALERMF LSFPT\TKTYFPHFDL\SHGF\AQV*G ATGKKVADALTNAVAHVDDMPN\ ALSALSDLHAHKL RV\DPVNF\KLLS H\CLLG*PWAHLPRPSSTPGGCTPS LGTNFLGFLCLKHRCLNLPNNL
2607	8104	A	2821	270	453	
2608	8105	A	2822	115	427	
2609	8106	A	2823	1	1656	
2610	8107	A	2824	1	1188	
2611	8108	A	2825	1091	1764	SIAYQPKRVQDQTDSPILPELISNF SKVSGYKIN/AKKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN AIPKLPMPFFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYQNSMVLVPK QRYRSMEQNRALRNNAAYLQLSDL
2612	8109	A	2826	1	1449	
2613	8110	A	2827	2	1675	
2614	8111	A	2828	301	453	
2615	8112	A	2829	1	2139	
2616	8113	A	2830	83	1257	WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAILSKLTQEQTCKHH

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						MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNLYIFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKTLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDKWDLIK LKCFCCTAKETTIRVNRQPTK
2617	8114	A	2831	1	1383	
2618	8115	A	2832	2	153	
2619	8116	A	2833	1	2436	
2620	8117	A	2834	1569	1835	
2621	8118	A	2835	933	2812	
2622	8119	A	2836	56	1692	KSKSKQHSKASRRQEITKIRAEKKEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDITT NPTEIQTIREYYKHL YANKLENRE EMDKFLD TYTL PRLNEEEVESLNTP ITGSEIVAIINSLPTKKSPGPDGFTAE LYQRYKEELVPFLKLFQSIEKEGIL PNSFYEASIIIPKPGRD TTKENFRP ISLMNIDAKILNKILAKGIQHIKKLI HHDQVGFIPGMQGRFNIRKSINVIQ HINRTKDKNHMIISIDAEKAFDKIQQ PFMLKTLNKL GIDGT YFKIIRAIYDK PTASII L NGQKLEAFRLKTGTRQGCP LSPLLFNIVFEILARAI RQEKEIKGIQ LGKEEVKLS\LFADDMIVYVENPLP SQPQNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIHLTRDVKDLAF KETYPKLLNEIKEDTNK WKNIPCS WVGRINIVK\MAILPKVNYRFNAIPI KLPMTVFTELEKNYFKVHMEPKKE PALPSQS
2623	8120	A	2837	2	433	
2624	8121	A	2838	371	452	
2625	8122	A	2839	307	497	
2626	8123	A	2840	95	314	
2627	8124	A	2842	2	311	
2628	8125	A	2843	1	602	
2629	8126	A	2845	571	690	CQQGFSFLQAYGPAQHAIS\MRKFK AKYPDYEVTWANDGY
2630	8127	A	2846	130	943	
2631	8128	A	2847	45	405	GIPGRRNMAVADLDLIPDV\DI DSD GVFKYVLIPSPLGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST
2632	8129	A	2848	1340	1504	
2633	8130	A	2849	3	200	GSCACAGSCKCKCKCTSCCKSEC GAISRNLGLWLR\CCSCCPLGCAKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AQGCICKGASEKCSCCA
2634	8131	B	2850	1	384	MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFWLWFSSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCACK AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT*
2635	8132	A	2851	1	2880	
2636	8133	A	2852	584	1253	
2637	8134	A	2853	1	2736	QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLOQKLETE RELKQRLLEEQAKLQQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALEKEKARCAELEELQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGQQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGAVGASELANTAKADVPIYILK MESHPTTCWPGRTLYLLAPSFDPK QRWVTALESVVAGGRVSREKAEA DAKLLGNLLKLEGDDRLDMNCTL PFSDQVVLVGTEEGLYALNVLKNS LTHVPGIGAVFQIYIHKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQDISPNIFEAVKGCHLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSIHFTNYSILIGTNKF YEIDMKQYTLEEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNPRYL PAISSGAIYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRG PTYNEHITKRVASSPAPPEGPSHPRE PS\HPTATARGGPSCAGTS\WPWPPG AREVPRPDAQHAERAVPREAV
2638	8135	A	2864	426	539	
2639	8136	A	2865	1	1134	
2640	8137	A	2866	766	1115	SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHGWRYAPDR*RSVR RCDGDPLHPDVRRRSG
2641	8138	A	2867	61	390	
2642	8139	A	2868	627	1324	
2643	8140	A	2869	343	452	
2644	8141	A	2870	589	672	

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2645	8142	A	2871	1	3000	
2646	8143	A	2872	2	191	
2647	8144	A	2873	251	505	GSSSRLGQRTD*ATASRRHF\KNKV PGEAKNCSPEDDEIPLYLKGGV\AD ALLYRATH\MILTVG\GTSICPYEL AVASFPPKAGS
2648	8145	A	2874	1780	1914	
2649	8146	A	2875	1154	1256	
2650	8147	A	2876	1	2629	
2651	8148	A	2877	334	468	YEEEEEDYD*EEEESEPPPLDENDL EEDVVFQPPQIEGEAVYDA
2652	8149	A	2878	2	416	
2653	8150	A	2879	1	4116	
2654	8151	A	2880	3	3080	EELEASKSFGPGNEEEEEKEEKEYE EEEEEDYDEEEEESEAGNQRLQQV MHAADPLEIQADVHWTHIREREEE ERMAPASESSASGAPLDENDLEEDV DSEPAIEGEEAAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EALELRVSEDEEKLPA SPKHQERG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPPEERLFPEPLL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSP LAVDEALRRSDLVEEFWMKS AEIRRLGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLPTPRSPSD RELRS AQEERRELS SSSGLGLHGSSS NMKTLGSQSFNTSDSAMLTPPSSPP PPPPPGEEPATLRRKLREAPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLPALEGTLPQKRG LPLVS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQ GKERRPDSPTRPTLRGS EEPTLKHEATSEEVLSPPSDSGGPDG SFTSSEGSSGKSKKRSSLFSPRRNKK EKKS KGEGRPPEKPSSNLLEEAAAK PKSLWKS VFSGYKKDKKKKADDK\ SCPSTPFSGATVDSGKHRVLPV\VR AELQLRRQLSFSESDLSDDVLEK SSQKSRREPTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYESEL MIFARELELEDQRS RLQQELRERMAVEDHLKTEEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAMLSKGFSLNWS
2655	8152	A	2881	1	4132	
2656	8153	A	2885	1898	2056	
2657	8154	A	2886	1	233	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2658	8155	A	2887	1092	1339	
2659	8156	A	2888	363	512	EPLEGLLCLEGKGVEIVTILQAETPG EPLPP*KPHS*PGLCLRYRGHTL
2660	8157	A	2889	1	136	
2661	8158	C	2890	12	236	MTPGGLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSGKIT *
2662	8159	A	2891	1548	1849	
2663	8160	A	2893	1	1441	
2664	8161	A	2894	954	1194	
2665	8162	A	2895	2039	2207	
2666	8163	A	2896	680	757	
2667	8164	A	2897	361	476	
2668	8165	A	2898	226	293	
2669	8166	A	2905	265	396	
2670	8167	A	2906	250	447	
2671	8168	A	2907	632	1038	
2672	8169	A	2908	3	363	VKDDPNDEHQQKRGHKPFLRELPR ATIFFLINL*VIAEVEVQDSCIDQAES EMLLRSGAPDPGVPL*GCFFALVIT HTHSSRAAMAFVPTGKKASCYSQE PS*WQNSPNDTQDHSNDLSE
2673	8170	A	2909	57	448	
2674	8171	A	2910	62	371	
2675	8172	A	2911	398	789	VTGAPLMLPVLPKPGMPLAALVTG LSGLLWPCCAEVGTGFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSTCAGSCKCKECKCTSCCK SECCSCCPVGC\SKCAQG\CVCKG ASEKCSCCD
2676	8173	A	2912	577	896	
2677	8174	A	2913	2	184	
2678	8175	A	2914	1	459	SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPPNPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRALWIDSDLRCAPLGLS TGGGKSRRIKGLGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLLQLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV
2679	8176	A	2915	440	620	
2680	8177	A	2916	2	987	FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTVWSPPGAE IRMFRFMRDVEPEDPMFL\MDPFAI H\RQH\MSRMF\SGGFWILAPFLSITD WQHCQGTRP\ASRR\MQQAGSCSPL FG/MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRSAPGG IRETRRTVRDSDSGLEQMSIGHIRD RAHILQRSRNHRTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQRP LEFRRLESSGAGGRRAEPPRLAIQ GPEDSPSRQSRRYDW
2681	8178	A	2917	121	329	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2682	8179	A	2918	323	457	
2683	8180	A	2919	1	243	
2684	8181	A	2920	147	321	
2685	8182	A	2921	1	2310	
2686	8183	A	2922	319	773	
2687	8184	A	2923	85	369	
2688	8185	A	2924	1	681	
2689	8186	A	2925	1556	1953	HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWRWQHPRGPGGPVSR RRPPHGGTPTGTVRRGGGGDPAAPG SGCPSPAVVPPRCPGAPLRRATLPP ACCGSLACSP*PAPS/TPPL*ADD SCSVGLPT
2690	8187	A	2926	322	376	
2691	8188	A	2927	365	666	
2692	8189	A	2928	310	448	
2693	8190	A	2929	908	1189	
2694	8191	A	2930	761	913	
2695	8192	A	2931	1188	1373	EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK
2696	8193	A	2932	240	475	
2697	8194	A	2933	1212	1424	
2698	8195	A	2934	403	539	
2699	8196	A	2935	436	594	
2700	8197	A	2936	1	570	
2701	8198	A	2937	1086	1359	
2702	8199	A	2939	40	361	
2703	8200	A	2940	12	337	
2704	8201	A	2941	232	339	
2705	8202	A	2942	951	1069	
2706	8203	A	2943	286	621	
2707	8204	A	2944	299	513	HKCYFTLAHVHLIISFCAATLE*A*P SWGTCSTPNFVNTTPTLAYYLGL WRSLRPFSDSVSFSFCGIL
2708	8205	A	2945	97	258	
2709	8206	A	2946	5	464	
2710	8207	A	2947	1	522	
2711	8208	A	2948	76	488	
2712	8209	A	2949	619	746	
2713	8210	A	2950	125	279	
2714	8211	A	2951	1300	1410	
2715	8212	A	2952	1867	1947	
2716	8213	A	2953	2	52	
2717	8214	A	2954	352	538	
2718	8215	A	2955	3	313	QEFGTRICPAACFPLESGTPGFSLAS KWTNCS CSPVGS\CACAGS\CK\CN RVANRTVLTQTSCSC\CPVGCABA LPRGCICKGTS\DKRSRCLDARDSC ALQM
2719	8216	A	2956	1172	1914	HFSAPQWASPCS/SLLLLGLEGQGIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCQPLVSSAVD RRAPAGRRTFLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQILH RVSLNILPPGAVEDDVQAGRWRVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SRDDVACGSEEEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNNPTALAKSKEELSMPKS YQY
2720	8217	A	2957	3	632	
2721	8218	A	2958	3	728	
2722	8219	A	2959	194	451	
2723	8220	A	2960	2	484	NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENSM KGNSIYF*GPGHDPLLMNIVY*KS LTINNHMHKIT*ESL TEVLFSQGIFS VTNPHEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA
2724	8221	B	2961	65	391	MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTOIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY*
2725	8222	A	2962	1	2148	
2726	8223	A	2963	816	1014	
2727	8224	A	2964	2	358	
2728	8225	A	2965	84	176	
2729	8226	A	2966	137	426	QACIMREYKLVVLGSGGVGKSALT VQFVQGIFVEKYD\PTIEDS\YRKQV EVDAQQCMLLEILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI
2730	8227	A	2967	449	602	
2731	8228	A	2968	203	535	
2732	8229	A	2969	2	446	
2733	8230	A	2970	3	240	
2734	8231	A	2971	914	1291	
2735	8232	A	2972	188	266	
2736	8233	A	2973	191	306	
2737	8234	A	2978	1	440	
2738	8235	A	2979	3	670	TSRGRVGTQAGEPRDLRPPPCSSPL RV\AVV\CLEQPERGAWEAHNIPQP NGDSA VRSFG\TGTHVKLP GPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIAG\RNKRIKP\GPERF QNCKDLFDLILT\CEERVYDRVGWK I*ISR\EQGDLPSVHVVNLDIQDNH EEATLG\ARFLICE\VCQCQHTTEYM HNEIDELLQEFEEKSGRTFLHTVCF Y
2739	8236	A	2987	367	492	
2740	8237	A	2988	49	332	
2741	8238	A	2989	582	923	
2742	8239	A	2990	523	668	
2743	8240	A	2991	942	1513	
2744	8241	A	2992	176	362	
2745	8242	A	2993	4937	5137	
2746	8243	A	2994	651	836	
2747	8244	A	2995	1686	1883	
2748	8245	A	2996	415	635	
2749	8246	A	2997	2	308	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2750	8247	A	2998	57	598	
2751	8248	A	2999	802	923	
2752	8249	A	3002	119	297	
2753	8250	A	3003	950	1314	
2754	8251	A	3004	1	579	
2755	8252	A	3005	27	483	RDAEDAIYGRNGYDYGGQCRLRVEF PRTYGGRGGWPRGGRNGPPTRRSD FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLRKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSRSGSRGRDSPYQSRGS PHYFSPFRPY
2756	8253	C	3006	34	171	MPKSFRVIAERSMHSWYVCFLICFIL HISITLHSLVMVFVTWREY*
2757	8254	A	3007	1688	1871	
2758	8255	A	3008	1	688	MSGWADERGGEGDGRIVVGNLPTD VREKDLEDLFYKYGRIREIELKNRH GLVPFAFVRFEDPRDAEDAIYGRNG YDYGGQCRLRVEFPRTYGGRGGWPR GGRNGPPTRRSDFRVLVSGPSPSG SWQDLKDHMREAGDVCYADVHK DGVGMVEYLRKEDMEYALRKLK *PPKFRSH\EGETSLHRRFIPERSNQL MATSPVSGLGSRGRDLSIPKARGSP HYFSSFPGP
2759	8256	A	3009	428	579	
2760	8257	A	3010	1924	2043	
2761	8258	A	3011	131	395	
2762	8259	A	3012	910	1173	
2763	8260	A	3013	1295	1489	
2764	8261	A	3014	1477	1604	
2765	8262	A	3015	443	805	
2766	8263	A	3016	1	2109	
2767	8264	A	3017	1297	1408	
2768	8265	A	3018	3	314	
2769	8266	A	3019	5	340	GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLGTGEPRVYIRNKV ANTGVPGAPGPSIGGVTPATDYCH RIAPILAARRRRRRRRRRRRRRRG GGGGVAGGGGGG
2770	8267	A	3020	1	1973	DGGARARGRAAARRRRRPRRRRRR RRRRRRRRRRRRRRRRRLGLERP QPTSRGRAPGASRAEEKMEELVVE VRGSNGAFYKAFVKDVHEDSITVA FENNWQPDRQIPFHDVRFPPVGYN KDINESDEVEVYSRANEKEPCCWW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLRVNPKNPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVILSINEVTS KRAHMLIDMHFRSLRTKLSLIMRNE EASKQLESSRQLASRFHEQFIVREDL MGLAIGTHGANIQQARKVPGVTAI DLDEDTCTFHIYGEDQDAVKKARS FLEFAEDVIQVPRNLVVIGKNGKLI QEIVDKSGVVRVRIEAENEKNVPQE EEIMPPNSLPSNNSRVGPNAPEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HLDIKENSTHFSQPNSTKVQGRGMVP FVFVGTKDSIANATVLLDYHLNYL KEVDQLRLRLQLIDEQLRQIGASSR PPPNRTDKEKSYVTDDGQGMGRGS RPYRNRRGHGRRGPGYTSGTNSEAS NASETESDHRDELSDWSLAPTEEER ESFLRRGDGRRRGGGGK\QGGRG RGGGFKGNDDHSRTDNRPRNPREA KGRTTDGS LQNTSSEGSRLRTGKDR NQKKEKPDSVDGQQPLVNGVP
2771	8268	A	3021	1	2116	
2772	8269	A	3022	656	883	
2773	8270	A	3023	303	589	
2774	8271	A	3024	2	478	MAGKQAVSASGKWLMGIRKWYY NAAEFNKLGLMRDDTIYEDVDKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCCSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLK\EVIRE RKERE EWAKK
2775	8272	A	3025	323	400	
2776	8273	A	3026	2	396	RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYY\NAARIQNKL LMRDDTIY\EDVDKRS*EDFPEN LYNDRMFRRH*EGHWTLNLKHQILP KEQWTF\EEKNFYLEPYLKE/VLF RERKERE\EWAKK
2777	8274	C	3027	144	341	MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNFLSFQGXQHKKNK TGQHFTSKCTEPFLQD*
2778	8275	A	3028	1070	1335	
2779	8276	A	3029	2	303	
2780	8277	A	3030	149	244	
2781	8278	A	3031	1642	1797	
2782	8279	A	3032	1115	1320	
2783	8280	A	3033	1240	1408	
2784	8281	A	3034	539	669	
2785	8282	A	3035	1155	1579	
2786	8283	A	3036	437	666	
2787	8284	A	3037	51	279	IKGRWEPPPLASFFLT SQGHCS DGP GP*GWGEAVSPRGRNTLSSSSWHW VPYSELRGRGVACRKEVYKIVQNT QH
2788	8285	A	3038	3	300	
2789	8286	A	3039	451	760	
2790	8287	A	3040	183	410	
2791	8288	A	3041	602	1145	
2792	8289	A	3042	2	496	
2793	8290	A	3043	710	896	
2794	8291	A	3044	143	601	
2795	8292	A	3046	120	280	
2796	8293	A	3047	2	424	
2797	8294	A	3048	3	452	
2798	8295	B	3049	240	420	XLKGHGQRKVAERADPKLPQRGR TCPKRRCPPLSDPARCTSFVRDPVN FQASLSHCLAW*
2799	8296	A	3050	310	401	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2800	8297	A	3051	544	700	
2801	8298	A	3052	1	568	
2802	8299	A	3053	686	787	
2803	8300	A	3054	8	182	
2804	8301	A	3055	227	547	
2805	8302	A	3056	1	523	ESLRKQLGQEPFF\DMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIKPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHWRLTQFPSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCRSRCS RNRSP
2806	8303	A	3057	919	1100	
2807	8304	A	3059	429	780	
2808	8305	A	3061	567	682	
2809	8306	A	3062	148	372	
2810	8307	A	3063	113	303	
2811	8308	A	3064	367	449	
2812	8309	A	3065	48	369	
2813	8310	A	3066	979	1254	
2814	8311	A	3067	173	776	
2815	8312	A	3068	1	111	
2816	8313	A	3069	33	494	
2817	8314	B	3070	100	154	MVHLTPVERVCRCYCPVGQX*
2818	8315	A	3071	559	775	
2819	8316	A	3072	744	940	
2820	8317	A	3073	1	255	
2821	8318	A	3074	1	1206	
2822	8319	A	3075	905	1823	
2823	8320	A	3076	36	689	
2824	8321	C	3077	215	325	MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLT*
2825	8322	A	3078	1	831	
2826	8323	A	3079	97	236	
2827	8324	A	3080	409	602	
2828	8325	A	3081	818	1095	
2829	8326	A	3082	528	714	
2830	8327	A	3084	91	242	
2831	8328	A	3085	75	430	VSPGLPAARLFQVAYLDShLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFFL CGPFKVVIICTELQNVSRSPQTTLAT VYCNKITSYICKKKK
2832	8329	A	3086	1000	1145	
2833	8330	A	3087	225	324	
2834	8331	A	3088	3	54	IIHYSLLIIV*CWVQF
2835	8332	A	3089	461	658	
2836	8333	A	3090	337	408	GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCDPPGRYPLRDSGQSRTLH AGSSATTIQEPRGA
2837	8334	C	3091	155	453	MLGALGAEELSLDSLPEGLLNFSKP GSERGGRLGLVPAAGEGPCDPPGR YPLRDSGQSRTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2838	8335	C	3092	121	393	MALPGRLPHRKLAGGTLEAPWPGIP SGAVRRHQPPPTTLXXWLGVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI*
2839	8336	A	3093	270	573	
2840	8337	A	3094	15	297	
2841	8338	A	3095	970	1098	
2842	8339	A	3096	127	296	
2843	8340	A	3097	875	1075	
2844	8341	A	3098	171	404	
2845	8342	A	3099	186	392	
2846	8343	A	3100	2	202	
2847	8344	A	3101	2	242	ARGNMAAATLTSKLDLLFRRTSTF ALTIIVGV\MFF\ERAF\DQGADAYFT DH\NEGVRPCAIPDLGTRLRGDSGV EKL
2848	8345	A	3102	79	1137	
2849	8346	A	3103	374	519	LDSRRK**C*LERSPHE*TS/DLSSGS LLI*GIWSILFYPMF*KFQKEN
2850	8347	A	3104	1	1214	
2851	8348	A	3105	105	379	
2852	8349	A	3106	260	421	LLYGDCTWTSFHLQRLQLHCQVSQ PCREL*LVSSVLCFFISEELHCVTG HF
2853	8350	A	3107	420	848	
2854	8351	A	3108	664	1059	
2855	8352	A	3109	73	269	
2856	8353	A	3110	307	566	
2857	8354	A	3112	316	410	
2858	8355	A	3113	200	403	
2859	8356	A	3114	258	377	
2860	8357	A	3115	1767	1893	
2861	8358	A	3116	1	389	
2862	8359	A	3117	3	569	RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTWQKFSSPTEVERCMES L\IAVFQKYAGKIDGYNNSLPRPE F/L*AFMNTLAAFTKNQEGPWVSL DRMMEETGTPNSDGSARISGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPLPGGGFQTPPFSPGLS VLHLPQAHPSLEAH
2863	8360	A	3118	362	712	
2864	8361	A	3119	2	152	
2865	8362	A	3120	134	760	
2866	8363	A	3121	670	891	
2867	8364	A	3122	44	63	SPSNRNTEEGTLTNIIHNLGMYVFL HAVKGTPTFETP*PG*KARAP*PPLGN NWDYGD\DRFTSFTGSFFTISPILYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQEH
2868	8365	A	3123	88	207	
2869	8366	A	3124	2	191	
2870	8367	A	3125	145	865	
2871	8368	A	3126	69	118	
2872	8369	A	3127	1148	1323	
2873	8370	A	3128	197	327	PLGKKFSCSKSLRLLGPFLQL*SLRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKTTY
2874	8371	A	3129	154	303	
2875	8372	A	3130	3	158	
2876	8373	B	3131	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2877	8374	A	3132	383	529	
2878	8375	A	3133	1981	2132	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNFHFASFLC\ASINKKWKRI
2879	8376	B	3134	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2880	8377	A	3135	383	529	
2881	8378	A	3136	1979	2131	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNFHFASFLC\ASINKKWKRI
2882	8379	A	3137	296	592	
2883	8380	A	3139	224	700	VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEEPFQIHLKLTFMFKNTT NFIFTAELCDQCQGL*NLIHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLFKSTMGKDQRQI DNNIMN
2884	8381	A	3140	761	963	
2885	8382	A	3141	475	715	
2886	8383	A	3142	381	698	
2887	8384	A	3143	2	235	YASLEPPDRPQVGASCGPGTYV*GA VPPSPAGVGREGVAGKGTGGCTCDK PLSPCSLAG\RRGSFPRRPSWTSPL LCW
2888	8385	A	3144	49	353	
2889	8386	A	3145	174	495	
2890	8387	A	3146	73	226	
2891	8388	A	3147	326	421	
2892	8389	A	3148	1306	1444	
2893	8390	A	3149	53	246	
2894	8391	A	3150	228	271	
2895	8392	A	3151	419	599	
2896	8393	A	3152	1	322	
2897	8394	A	3153	151	375	
2898	8395	A	3154	2017	2191	
2899	8396	A	3155	3	234	LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLLQGLSLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR
2900	8397	A	3156	43	408	
2901	8398	A	3157	3	374	
2902	8399	A	3158	1	823	MAVVAPRTL LLLLLSGALALTQTWA GSHSMRYFSTSVSRPGSGEPRFI GYVDDTQFVRFDSDAASQRMEPRA PWMEQEEPEYWDRQTEISKTNQI DLESLRIALRYYNQSED/VPPPKTH MTHHPISDHEATLRCWALSFPYPAEI TLTWQRDGEDQTQDTEL VETRPAG DGTFQK WASVVVPSGQEQRYTCHV QHEGLPKPLTLR WEPSSQPTIPIVGIL AGLVLF GAVIAGAVVA VMWRRK SSDRKGGSYSQAASSDSAQGS DVS L TACKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2903	8400	A	3159	1	1264	MAVMAPRTL L L L L L SGALALTQTWAGSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDQETRNVKAQSQTDRNLRIALPLTYNQSEAGSHTLQMMYGLGRGGS DGALSFRLPPVTA YDGKDNIALNEDLRSWTAADMAAQITQRKWET/AAHEAEQWRAYLEGRVVEW\LRRYLENGKETLQRTDPP\KTHMTHHPISDHEATLRC\WALSFYPAEITLTWQRDGEDQTQ\DTKL VQTRPAGDGT\HKGASCVGPLGEEQRYTC\HVQHE\GLPK\PTSMRW*PSSQPTHPPSWG I HCLALVLLWKL*SLEAVVAACECGRRKSSDRK\GGSYTQAAKPV TSAQGS D VSLTACKSVRQLPCVGLRGKSCFLPFPLVDLEEPWTLFPAKGT LHVSVFM
2904	8401	A	3162	1	342	GSRTVPSPSPSSGLASPGSPTHRSLGPTTPPMASATEDPV LERYFKGHKA AITSLDLSPNGKQLATASWDTFLMLWNFKPHARAYRYDGHKDVVTSVQFSPYGYLMAAG/SRDLSVRLWIPV**EYS*NGKQLATASWDTFLMLWNFKPHARAYRYDGHKDVVTSVQFSPYGYLMAAGLETYP
2905	8402	A	3163	1	583	DMESRSVTQPGVQWCYLG*LQPPP PRF*RFSCSLPGSWDYRCVPPHPANFFIFSRDGVSHHVGGAGLELLVSSDPPASASQSAGITGLSHHARPD/YTFLLTVFEPFHGTHVRPPVTCGTLASNWTPTAFISLAENTKV LKVALKEVPFGFDIAISKASGT VQIRAMSFMKTTFLSPSFVRECHTHDHVTLLQS
2906	8403	A	3164	1	347	FFILFFLRQSHSVA*AGVQWHNLDLSLQPLPPGFKQFS/LSLPSSWDYRRMP PRPANF*FLVETGFRHVGGAGLELLTSGDPPASTSQSAGITGVSHGAQSCPLLYIEFPLSILAAT
2907	8404	C	3165	13	399	MEKIPVLFRVANLISIIPAPNKSRLCGKTRISRSASKANTRVFLACRFGLAGDNAIANVHAPDADLEAQSDVERTMDLKPCIWVPDTLGEAEQTAPADRLSMHTQHFGRRPRADHEVRRPRPSWLIW*
2908	8405	A	3166	168	414	NPLLLPNTFPANGNTILIKEKVLFLFF*DGSPVLSRPDCGLQWRNLG\SLQSPPPGFTPFSCSLSPSSWDYRHPPLRPANFFLYFLVETGFHRASQG\GLDLLTSRS/IPPRASQSA/RGLQGVSHPRPAYMSLRYNKPAHVPLKIKVKK
2909	8406	A	3168	28	123	
2910	8407	A	3169	2	123	ENRLMAGGE/HMLAAILLFTALRCLCKVKHKPGLHAH*GTAP
2911	8408	A	3170	1	402	QGFSPPESLRYG\SWEGKALTFFQPDTHKGSVLED**KRKASLQLR*EEGICL\CLSLGMECLGVKP/VAYILFTEIGESRLMAGGK/HMLAAILLFTALRC

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						LGKVKHKSGLRAHRGTAPFLKLIY DTESFAHMFSC
2912	8409	A	3171	1	399	SSSLQPPPP\GFK*FSCIGLPTSRDYR CVPPRPANFVFSVETGFHHVQGAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWSCNSLFTGENVI EANQNLLALRFISAMDQLSLRIVRN QTFFF
2913	8410	A	3172	1	451	LYGEGWSFALVAQAGVQWCDLRL LQPLPGFK\YSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCSLPSS*DYRCTPPGLA*/F FIFLVEMGFSLRLVSN*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR
2914	8411	A	3173	2	346	
2915	8412	A	3174	1	2430	
2916	8413	A	3175	576	983	GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSFAFKKVNLSLST*Q FKYKNKGICAAACQFSLFPLK*PIRL FFAGEHTIRNYPATVHGLLSGLRE AGVRIADQFLGAMYTLPRQATPGVP AQQFPKACETDAF
2917	8414	A	3176	1	2930	RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKKAIAAAAAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPPGSAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDLANLSEDEYYS EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGAAFQSRLPHDR MTSQEAACFPDIISGPQQTQKVFLFI RNRTLQLWLDNPKIQLTFEATLQQ EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIIIGSGVSG LAAARQLQSFGMDVTLLEARDRVG GRVATFRKGNVADLGAMVVTGL GGNPMNAVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQLDNFVNLNNKPVS LG QALEVVIQLQEKHVKDEQIEHWKKI VKTQEELKELLNKMVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVSKS HRDLTALCKEYDELAETQGKLEEK LQLEANPPSDVYLSSRDRLQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGVEIAVN TRSTSQTFIYKCDVLCCTLPLGVK QQPPAVQFVPLPEWKTSVAVQRMG FGNLNKVVLCFDRVFWDPVSNLFG HVGSTTASRGELFLFWNLKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRS\SAVPQPKETVVSRRWA DPWG\RGs*SYVAQGS\SGNDYDL MAQPYHSWAPSIPGAPQPIPTLLC GENITIRNYPS/TPVHGALAEVGSRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AGKEIARPSFWGAMY/TRLPRQATP GCFLAQQVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD
2918	8415	A	3177	62	447	GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPNVHSHHTHTHT HTHTHTHTVSYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ
2919	8416	C	3178	90	233	MRIGYKVKDGTFLDLQMGGLPGXX XXSRPKRNHQLSKGEREINLGKL*
2920	8417	A	3179	462	929	SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNHPQIMPLFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FSCLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGGAGLELLAS SDPPASASHSVGITGVSHHTWPMPL LLI
2921	8418	A	3180	160	272	FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLP CPANFSYFL*RQSLTVLPRLVNSW TQVSLLTQPSVLGLQA
2922	8419	A	3181	6	270	RDRVLLCHTDWISAVESQLTASSN SW\VK*SSCLSLQRTDYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV
2923	8420	A	3182	92	549	VWQGLHPQLHPHFASQNLIQSLALS LKAGV\QWHDLSSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLQCFSNSS RLEHTDGIHFLSEAMSAIHESFPHI
2924	8421	A	3183	16	661	DRVSVTQAGVQWCNLGSLQPLPPR FR*FSCLSLSSWDYRRPPRPANFC IFSRD/MAFTTLARLVSNS*PQ/CDPP TSASQSAEITGVSHRAWVLSPPQPF FFF\DMESHAIQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPR PANFFVFL*\RDGVSPC*PGWSRSPD LVHPPWSPKSAGITGLSHCAQPYP QFSKHKDLRVSGKA
2925	8422	A	3184	288	489	CGLILELEKLLL VWIQIQMSLNKA TI*SNDIFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG
2926	8423	A	3185	3	166	WLYSANVAHAPYRGSALWCLRDS RPPAQYWSAFQHYSL*PTQFPLEFT TKSLLS
2927	8424	A	3186	3	725	LALLGRVYDVLSDARD/YVELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLQEKQ TFPPCNAEWSSARGSRWCSQKSPK DADDTSIYMFYQKVGDNIDSWN AGRVFKDSDKFDANDPILKDQTQE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNGVKPEGTTETTMK
2928	8425	A	3187	1	1988	
2929	8426	A	3188	134	944	MLRCGGRGLLLGLAVAAAAMAA RLMGWWGPRAGFRLFIPEELSRYS GRPR/DPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRAV TGDCSEAGLVDDVSDLSAAEMTL HNWLSFYEKNYVCVGRVTGRFYGE DGLPTALTQVEACDSTRGFGGQT NYKLQEKQTFPPCNAGGGAQPGAA RLWCSQKSGVSRDW/ALAVPRKL YKPGAKEPRCVCVTRTGPPSGQMP DNPPHRNRGDLADHPNLAETGCPP LAITCSFPL
2930	8427	A	3189	1	312	AQPGVQ*RNHSLQPPPPGSKRLSC LSLPSS*DHRPPPCANF/SVFLVE MGFHHVGQAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR
2931	8428	A	3190	2	176	
2932	8429	A	3191	3	67	
2933	8430	B	3192	1	1587	MVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLKRVINTLADHH HRGTDGFGGSPWLHVIIAFPTSYKVVI TLWIVYLWVSLKKTIFWSRNGHDG STDVQQRAWRSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVITLRRH VETKVRKIRKRVTTKINHDKIN GKRKTARKQLSQHSISHVLAFS DPP FCKKGSLLQAPPSADDNIKIPAERLR IPLPPSADDNLKTPSERQLTPLPPSAP PSADDNIKTPAERLRGPLPPSADDN LKTTPSERQLTPLPPSAPPADDNIKT PAERLRGPLPPSADDNLKTPSERQL TPLPPSAPPADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPPSAPP ADDNIKTPAERLRGPLPPSADDNLK TPPLATQEAEEKPRKPKRQRAAE MEPPPEPKRRRVGDVEPSRKPKRRR AADVEPSSPEPKRRRVGDVEPSRKP KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS *
2934	8431	A	3193	792	1024	SHRKMFOQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPRT LH
2935	8432	A	3194	1	1656	
2936	8433	A	3195	112	368	SHRKMFOQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQMDTFFSLQ LCAQARTGRSD
2937	8434	A	3196	1	1353	
2938	8435	A	3197	1	452	
2939	8436	A	3198	1	510	
2940	8437	A	3199	2159	2958	

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2941	8438	A	3200	350	927	LFLVSPLKTISGSRNG\HDGSRDVQQ RA*SSNRRRQ\KKRVSSFRGNKIVLK DVITLRRHVETKVRAKIRKRKVTTK INHHDKINGKRRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQMDTFFSLQ LCAQALQREMAERKAAAYRHHSPIP VGNRVVQKHLHPHPVGPLI
2942	8439	A	3201	1	277	FFFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWGYR\RLPPCP AFILFYLF/CRDK/SLAMLPRLVLNS\ WAQVILPLQPPKVLGLQA
2943	8440	A	3202	1	340	SIHLPKAPPPNHSTGVWVQHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHLSSLSSWDHRCAPPHL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM
2944	8441	A	3203	2	354	ESLTGVQWHE\FASLKPL/PCLSLPR GWDYRRAPPRPAYF/*FLVETGFHHI GRAGLKLLTSDDPVVSASQSAGITG MSHRAWPLLKYFSALQTLNILQKN KNKNLIKTYFISLHVKIF
2945	8442	A	3204	166	373	EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPH TTL H/TALNI*SCPCCLFIFLVC
2946	8443	A	3205	2	775	LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAVPGRSNGSALTPVWV LIAKQSPPIVKILKFGWFPIILAMVIS SFGGLILSKTVSKQYKGM AIFTPVI CGVGGNLVAIQTSRISTYLHMWSA\ LGVLP LLMKKFCPNPRSTFC\SQKL NSMSCSRL LLLGGSQGH LIFFYIY LGGGVQSQ*T/TPDL CGCSNLLGRA* SRVTNPAVTGA EVELVRLTWHQGL \DPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY
2947	8444	A	3206	2	348	IAFGRYELDTWYHSPWPPEEYARLG RL\HMCEF*IKYMNSLTILTMHMVN CAFDPPPLGLPKELSLETRMETFFPAL PSFHSIHCPLCVQPELGKAFGCLSVG AWGCRTHLRFTGLH
2948	8445	A	3207	1	1503	
2949	8446	A	3208	1	635	
2950	8447	A	3209	1	665	MQAIKCAGGWKAEAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDTSGQKDYDRVT PPYPYPA/QADVFLICFSLVSPAS\FE NVRAKWYLNVRHHCPN\TPMILVGT \KDLRDDKD/TRIEKLKEKKLT\PIT YPQGLAHG*GRLGAVKYLG/CAPA AHTSEGLKTVFDEAIRA\VLCPPPVK ERGRENCLPVVNVSAPSFLGPVPLE PL
2951	8448	B	3210	1	693	MYGVSAFVVLSP TGR LPSVLQKEN QQQGV P NSPPLHEQM QMDTGLCRL TPGLTLAGQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS

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						RESCGERECVQFSQRTARDRWCI RAELEQDILDSAAVTIIQKWHIKGR ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEA AVRCKGPTRPAV ELPPRLPVLS*
2952	8449	A	3211	1	627	FFFGKSILLFKKINVTFDIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQOGETPS LLKNIKISRWWQAPVIPATREG*/ E*GESPEPGEGKVCRRAEIAATCTP AWGVQSETLSSKKKKSFLNVPHH PRQASVSFHCFFHKNQWGSPLWKKA RTFLLLGNGWLSCPHLSTQGNLSA PHLAEAQTLSP
2953	8450	A	3212	114	411	EREF RVPQVELQGPDLG*LNLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHVNQVGFELLT*GDP P/AWASQRVKMTGPTHQAHLEGNF F
2954	8451	A	3213	48	1400	HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDS\LLQPLTSAM/PPSAIPTP QRTSTPGLALFPGLSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTL VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYT\STSVPISSLAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSTPIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSSSTAATS TSLPHPSSTA AVLSGAFCFSTSPAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGQLAPS TVAAVTPLPVGWPQHPQLPVLPGF GSAFSFHNSRSWLHKPGFIWDFK AGRQFWFFRAFGPSRVSLGFLRLH NHPCKNYSIMRLHSQHCHYSRSIQLR LWESYPAQPDGVS
2955	8452	A	3214	2	694	QLLNYAPGPGGPRYVDCDLF*NGY HL\WYHD\YGHLEF\RLQLATQFEN WYMKYQSPIIQTKYG\AETVSGFPR DPPSDVPVRCPRKSLLEQ\YHLGLDS KPQKNTCLESPLWNF\ADFMTE\QSP \TKVLGNKKGIFTRAETTQSSAFL LRERY\WKIAQ*NPGIPHSVARSQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLLDCSRQTRTFSGLGfV VIYSSREH
2956	8453	A	3215	2434	2765	GIILFWAQLFPASFFFFF*DGVS LCPGWSAVVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLVLS*AS*VHPPWPP QSAGDYQA
2957	8454	A	3216	2	481	LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCPQAPGSSKSDCS

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						PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR
2958	8455	A	3217	126	364	RAWAN\LS*LKVLPPGLKGFSGLTL PSTGNNGLVPPPRVNFGSFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGIN PFFL
2959	8456	A	3218	132	342	SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLLVLPKRWDYRHEPLRPDLK
2960	8457	A	3219	2	264	QLTATPPPTGFKQFSCLSHPSSWDY RYVPPRPAKFCIFS/VRRGFTMLAR MVSIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVGQDGLN LLTLRSAHLSLPKCWDYRRKPPGLA CFMILNSYL
2961	8458	B	3220	134	3038	PGMEDGSDDMDTSVEDIGGRSCVT RFVRTLLIMEHGVKPHSKHLTEYF AFLYEFKMGEEESQFLSLQAIST MVHFYMGTKGPENPQVEVLSEEEG EEEEEEEDILSLAEKYPAALEKMI ALVALLVEQSRSERHLTSLQTDMA ALTGGKGFPFLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLA VQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAAYLLVS LIPSNFRQMFSTRSLHIPTRDLPLS PDTTVVVLHQVYNVLLGLLSRAKLY VDAAVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFPQKLSEP AIATNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGA VEELFNLMLQFIAQRPD MREEELEDIKQFKKTTISCYLRCLD GRSCWTTLISAFRILLESDEDRLLV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLLTLL NSYSPPELRNACIDVLKELVLLSPH DFLHTLVPFLQHNHCTYHHSNIPMS LGPYFPCRENIKLIGGKSNIRPPPEL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKFTE TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQLDSA TEKLTPRGKKPKERKTKDDEGGNS HLKGRAC*
2962	8459	A	3221	2170	3139	DLRALALLSVHTPKQLNPALIPTL QELLSKCRCTCQQRNSLQEQEAKER KTKALALWTTIITFRVGGGNTLGV TGLRVVCSAEPK*YKC*KQN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEEHTVDSCISDMKTE

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						TREVLTPSTSDNETRDSSIIDPGTE QDLSPENSSVKEYRMEVPSSFSED MSNIRSQAEEQSNNGRYDDCKEF KDLH\CSKDSTLA\EEEE\FPSTSISA VLSDLADLRSCDQALPSQDPEVAL SLSCGHSRGLFSHMQQHDILDTLCR TIESTIHVVTRISGKGNQAAS
2963	8460	A	3222	3	344	PESHAAQAGVQWPDGLSLQLSLP AFKQFSCSLPSSRDYRRASPRPANF *FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLPLKSPQ
2964	8461	A	3223	1411	1741	GYLQFSFSFFLFFFFFFFLLGESHSV T/RGLECSSVISTHCNLRPLGSSDSR ASASRVARTRGMHHHTRQIFV\LV QMGFH\HVGQAGL/DSS*PSVVHPP\ RPPKVLGLQA
2965	8462	A	3224	361	462	RHFLSTETYCNSFF/RHSSSKNYTK LKRYE*VS
2966	8463	A	3225	3	89	
2967	8464	A	3226	1	336	VCQVCGFRSRLHTNVNRH\LLLNKP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSEGIYLCQYCEYSTGQIEDLKI HLDKFHSADLPHKCSDCMLRFGNE RELISHLPVHETT
2968	8465	A	3227	951	2075	RTANLNFCILDKSQALNVNCPAET GL*LRANSRWP/PINCELCEFNSKYF SDLKQHMLKHKRTDSNVCRVCKE SFSTNMLLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFR\DPP\ HWCEQCDVQFSSSELYLHFQEHSC DEQYLCQFCEHETNDPEELA*\HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGFSSNTWKRKRKGQKTFPLLI NLELSTSLTNRYGSPWASELSTSVE VSMAMLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCSPPALIAQPI VGAQE
2969	8466	A	3228	2	415	LDPGSLAGFTSYIQFMYDEFVEEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHCVSITEMES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN
2970	8467	A	3229	607	1317	
2971	8468	A	3230	260	535	
2972	8469	A	3231	246	985	KLRHKMAANKPKGQNSLALHKVI MVGSGGVGKSALTLOFMYDEFVED YEPTKADSYRKKVVLDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITEMESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR

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						PAPVSRKTAHWAEEVFFDLRMREIRA RKMEDSKEKNGKKKRKSLAKRIRE RCCIL
2973	8470	A	3232	1	634	MAANKPKGQNSLALHKVIMVGS GVGKSALT\AQFMYDEFVED*E\PTK ADSSRKKVVLGDGEEV\QIGYPLDTA G\QED\YAAIRD\NYFRSGEGFLCVFS ITEMESFAATAEFREQILRVKEDEN VPFLLVGNKSDLEDKRPGL*EEAK\ NRAEQWNVNYVETSARKTRANVDK VFFDLRMREIRARKMEVEFYVLNGTK NTKRLAERIREGGCIL
2974	8471	A	3233	314	373	
2975	8472	A	3234	1	2129	PSVAGAATLWFHVTLPFCARLCGR RSCTHSGIITEFHFFHL/PFRPIPLAC GNDDCRIHIFAQQNDQFQKVLSCG HEDWIRGVEWAAFGDRLLLASCSQ DCLIRIWKLYIKSTSLETQDDDNIRL KENTFTIENESVKIAFAVTLETVLG HENWVNAVHWQPVFYKDGVLQQP MRLLSASMDKTMILWAPDEESGV WLEQVRVGEVGGNTLGFYDCQFNE DGSMIIAHAFHGALHLWKQNTVNP REWTPEIVISGHFDGVQDLVWDPEG EFIITVGTDQTTRLFAPWKRKDQSQ VTWHEIARSQIHGYDLKWLAMINR FQFVSGADEKVLRVFSAPRNFVGKF LCHYRKSLNHVLCNQDSDLPEGAT \APALGLSNKAVF/LREDKAPQPPDE EELLTSTGFEYQQVAFQPSILTEPPT EDHLLQNTLWPEVQKLYGHGYEIF CVTCNSSKTLASACKAAKKEHAAI ILWE\TTSW\KQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDSNLVIVEK AWIQS/TPEFEPVFSLFAFTNKITSVH SRIIWSCDWSPDSKYFFTGSR\DKKV VVWGECDSTDDCIEHNIGPLPPSVL DRGWGCDQLSASAQCSHPSQRYVV AVGLECGKDLLIYLGKRLIKFQK*M T/ATHCVGNKSKPKVIHWAIQKIYC WEGICSGKT*TRREGRR*VVYTFA SCG*DHTVKIHRVNBKCAL
2976	8473	A	3235	451	778	GSGRWKSRVARAGMQISGAHLQL NCKPPPPGLKADPPWLSL\SSWDP QMCPPTPWLLFVCLVETGFTMLPQ AALQLLS*SDLSA*ASQNAGITGMS HHAGPDTVPLF
2977	8474	A	3236	1	186	FFFEMESRTVTQAGVQWHDLG\SL QPP\PPGVSSDSPVSASHVAEITGAHH HTWLIFFIFFL*GVQWHDLGTLAT SSLLGSSDSPVSASHVAEITGAHHH TWLIFFIFFL
2978	8475	A	3237	1	353	KIWLFFVFKTDVSILVHPRLECSGAI SAHCNLHLPGLSDSHSAFRVAGTT GARHQAQLIFTFLVEMGFHHVGH GLKLPT*EIRPPRPPEVLGLHACAT VPGHKYVNEPIKMVLLK
2979	8476	A	3238	3	453	GQTGTWQGN TGQRVPQLPPHPPPIH

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						LVSRHRGKLRHGFLRPMPEPRGLES GKTGSARGVAACTSP*GRSG\QGGG PRDIAQQGGCRGSACGRSHEALRP RVWCGEGPQWTWCAVCP\NRSAP GAGLAD\RQHPGESRAWGETRLCE AGGAE
2980	8477	A	3239	232	472	LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQLTVTLKSR\VK*SSCLS/LP SSWGYRSVPPCPANYFYFL*QRQLT TLPS
2981	8478	A	3240	2	345	MVHVAVAGLNGTHSCPPASSSVLTF GHP\PHQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDFIPH DPAPPLLLSASWV
2982	8479	A	3241	205	361	DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSGRL\IPHDPAPPLLLSAS WV
2983	8480	A	3242	137	959	IPFPVMLDPAGROQQRWGRIMGY KVSLGGA*NLGRCKNIHKGSCREGL CLISLRAWEGRVLGEGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARA WCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGLE*TQPGLGYEHLKPFP/PSA PAA*PPG\PAKAQAPRKSCAPT VTH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFSPNAPLSPSPHP TTFPEFPCSPTPPPQIPHQDFPRS
2984	8481	A	3243	23	438	SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\VAQVVVQWHDRGSLQPQ TPGPK\YPPATAS*VAGARLIFFK*FL *RWDLTIMPKAGLKL PATGDPPACL LLSFLIPTGGFTRFEPTRHSLLEV GLSPMLVRHWLWA
2985	8482	A	3244	1	1061	ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADV\LFKIAPAVV HIELFLRHPLFGRNVPLSSSGSFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKSDIATIK IHPKKKL PVL LLGHSDRTCRPGEVL WVAIRQIPSP*QNTVVTGIVSTAQR EGRELGLRDSMDYI\QTDAI\NYG NSGGPLVNLDGEVIGINTLKV TAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNSIDFPE VSSGIYVQEVVPNSPSQSGGIQGGDI IVKVNGRPLVDSELQEA VLTESPL LLEVRRGNDDLLFSIAPEVVM
2986	8483	A	3245	1	268	QGSPSRDPSPLGGPNGGIFLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF
2987	8484	A	3246	20	353	KEVGRLTHSVNHSGGREKYVWHP GNAL*Y\GKLPVLP CIFIVNR*VQ*P *PERHMTVRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL

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2988	8485	A	3247	2	322	KLDNSSKWLENGTFDLSILQDLDFNFC*KMGKWSEVPYVQAFF\SIHSLPSLCSQCHL/CPDFPSFSP/YPLLLSPPQTQSPLNPPFPLTPLTSLLPRLLLARLNQVPILP
2989	8486	A	3248	141	924	PFSSQTVKLSGGATRNPVSSPKASGGQPSEGWEVALEGDSALMRQQCPGLLSRK/RAPGNPTASGS\APGATKRSLSGGRARRGLEFVVSRRFFGGGRAQSSLGNAHPHSGTIPKAPHASQQGLGLRLGGLEPSTPPVWHPPARPRASPDPSRVAGSPRSLPNPPAAGKGGRGSGEEARYFDLS*ILKSLPYPGHERVYQEPQRGVKTSCSCSPF/HLPLLLFQSSPPPSTLVGAGLKIGFLRCPVGGILIGKGFFFNCLHST
2990	8487	A	3249	1	363	QVSLVINWDLPTNR*NYIHR*AYIWNTPLPLHTWPSLGLKLLIFLIPFLEFQVGRGGRLDRKGGAINKGTEYDERTLRDIETFYNTSIEEMPFNVADHMLMGCPATQPLSGLIIGASDQY
2991	8488	A	3250	1	87	LNETVLLWHSGWMSTVVQTQLLPAASTWVVKQSSHLSSLNSWDHSRVP PHWANFLIFCR/DRSFAMLPKLVSNPWAQAVLPPLPPIVL*LNETVLLWHSGWMSTVVQTQLLPAASTWA
2992	8489	A	3251	3	270	CFNSAWTEPGARSPRPAAHSQPSVTSSPHPRTA\PRPPPLQR\PSF*SPP*RPRPP/PHVRHNYPSGLKSHH*SAE*PGPLGPIPTVY
2993	8490	A	3252	3	452	
2994	8491	A	3253	1	477	TLLVPQDSERTHPWCLSPADKTNVKA\AWGKVGHAHAGEYGAEALERMLFSFP\TTKTYFPHFD\LSHG\SAQG*RAHGK\KVA\DALTKAVAHVDDMPKRRCPP*SDLHGAQAFGWDVPVQLQSS*SHLPCLGEPWAAHLRPSFNPWRLQRLPWGQISWGFC
2995	8492	A	3254	3	295	LFLFFFFFF*MESHVTRLECSGTIWAH*NLHLPSSSDSPALASRVAGTTGMCHHIQLIFFVFLVEKGFHHVG*/DMSLSLDLVIHPPWPPKVLGLQA
2996	8493	A	3255	306	519	GTRVERHSRERPSCHLLCEPSQRYSPLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA
2997	8494	A	3256	453	626	HGSCLLHHREQVPIPPGIPNLSDSIL*FPVLRIWMLCLYTSCMWFSSQFWIAVMYFV
2998	8495	A	3257	1537	1909	NVLTVEDHPIPIPSKNRPFHNLLPVNLAFFFFFLNRVSF/CHLGWSAVARSHLTCNLLSPGFKQFSCLSLLSSWDYQACMHHTRLVFGVFSRDGGFTMLARLVSNS*PQVILPPLPPKVLGLQA
2999	8496	A	3258	1	342	KTESHVAQAGVQWCDLGLSQPPP PRFKLFSCLSLLSSWDYRGALPRPTDLFA/QFLVEMGFCHVAQAGLELLSSGNLFASASQTARITGVNHHTWPVL

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						*F*VKKIPPSLPGLL
3000	8497	A	3259	1	338	FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFSCLSLPNS*DYRCPPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRYLLRRRQ CLRQGLCRASVF
3001	8498	B	3260	188	1504	MRTLPPALLTCWLLAPVNSIHPEC RFHLEIQEEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTVP CPKVFSNFYKAGNISKNTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVLSMLATGSHLCLF RKLHCTRNHYHLNLFSLFRAISVL VKDDVLYSSSGTLHCPDQPSSWVG CKLSLVFLQYCIANFFWLLVEGL YLHTLLVAMPLPRRCFLAYLLIGW GLPTVCIGAWTAARLYLEDTGCDW TNDHSPVWWVIRIPILISIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLIPLFGVHYMVFAVFPISSK YQILFELCLGSFQGLVVAVLYCFLN SEVQCELKRKWRSCPTPSASRDYR VCGSSFSRNGSEGALQFHGRSRAQS FLQTETSVI*
3002	8499	A	3261	1	1047	MVSISWPRDLPASASQSAGITGLIGA LVLSVGIIAEVER/HEI*NP*KCLPGS SHHPHPGRRHVHGLLHWCAGVPP *QPPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTRGIFETKFLSQIE SDRLALLQVRAILQQLGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTVGVDGTL YKLHPHFSRIMHQTVKELSPKCNVS FLLSEDGSGKGAALITAVGVRLRTE ASS
3003	8500	A	3262	178	568	IFFFFFFFKMESCSVAQAGVQWWDL SSLQPLPPGFMPFCLSLPSSWDYRR PLLPANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE
3004	8501	B	3263	776	5218	MLGDNSSMSVTAPKTFQWDMMW RRKGLILILALCRPKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDQLDT MLWDSSTNLNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIIFVPVPQLKSFKQTQVQLRR ILPKPTQKSTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKIHLEAQQNNVEHKVEPFS GVYKKLMGKDVNFEPFQLMPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLRYNVMLENYRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS

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						FQKVLLRKYEKCGHENLQLRKGCK SVDECKVHKEGYNKLNQCLTTAQS KVFQCGKYLKVIFYKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKTQ HKCVYITEKSCCKCECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIICAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKEKGKFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTCHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKEKGKAFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFSRSTLTCHKTIHTGEKPY KCKEKGKAFKHSSALAKHKIIHAGE KLYKCEECGKAFNQSSNLTHKIIH TKEKPSKSEECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFSQPSHLT THKRMHTGEKPYKCEECGKAFSQS STLTTHKIIHTGEKPYKCEECGKAFR KSSTLTEHKIIHTGEKPYKCEECGK AFSQSSTLTRHTRMHTGEKPYKCEE CGKAFNRSSKLTTHKIIHTGEKPYK CEECGKAFFSSSTLNGHKRIHTREK YKCEECGKAFSQSSTLTRHKRLHTG EKPYKCGEKGKAFKESSALTKHKII HTGEKPYKCEKCKAFNQSSILTNH KKIHTITPVIPLLWEAEAGGSRGQE METILANTVKPLLY*
3005	8502	A	3264	1	208	RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLPRLVLN SWPQVTLLPQPPKVLGLQV
3006	8503	A	3265	78	359	RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLCLFLMLLTKL PTIIHRTVDAHSLADDDVE
3007	8504	A	3266	48	330	VCGCVWMLRVLFYCPGWSAVAQ S*LTAALISL/VNPSSSLSLPSSWDHR RAPPRPANFFNL*RQELPMLRLVL/ NVWAQVILPPWPPKMLELQV
3008	8505	A	3267	200	1033	RSLAPRWHLGHKEKNVTTSVWG WPSPGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME

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						PLCNGNLPTSMHTLG\HLHGVSNPSPQCTYTGESQLTEVLQNLGQR/RNIHNSRLNRLAPRM/LQSFQKEPRPSWVL/CPAWQALYW\RV*RPKERRPIELPSAQRLHYGP/PQMKDVP\ISLANILPQLPSSGNDVIVATHGQ*SLHHTLL*TPFHLGNVYVAMEEFKALVWYESTL\SLQPEFVPAKNRIQTIQCHLM LKKGRALLP
3009	8506	A	3268	2	2956	LADSSPSNLQIIKELLSMHHQPDPA LTKFDYLPVDSRSSSGFVGLRNG GATCYMNAVQQLYMQLPESLL SVDDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFFTSLIDQMDEYL KKMGRDQIFKNTFQGIYSDQKICKD CPHRYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCISLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGRSVDQ GGGGSPRKKVALTENYELVGVIVH SGQAHAGHYYSFIKDRRGCGKGK WYKFNDTVIEEFDLNDTLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQRVSDQNSPVLPPKSRVS VVRQEAEDLSLAPSSPEISQSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMVRDENLKFMKNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLLQAIQFLFQTYLRTHK KLRVDTEEWIATIEALLSKSFDACQ WLVEYFISSEGRELIKIFLLECNVRE VRVAVATILEKTLD\ALFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQIRAGDLLRHS ALRHMISFLLGASRQNNQIRRWSSA QA\REFGNLHNTVALLVLHSDVSS QRNVAPG\IFKQRPPIAPSSPLLPL HEEVEALLFMSEGKPYLLEVFMFAL RELTGSL\ALIEM\VVYCCFCNEHF SFTMLAFHLRNQL\ETA\PPHEFKGI RFPTTFMEILVIEDPIQAERV\KFVFE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHH\KMSDLYWTPLSNVS NETSTGKTF*RTISDHDTPYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPLDDWVSLRSDLDDVDP
3010	8507	A	3269	68	301	NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIP*IFRRLFVL*KL/ENS ILKYIWTCKGPRLVKTTFKNNSES W
3011	8508	C	3270	224	518	MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXX*
3012	8509	A	3271	342	724	NTYPWAVL/VFFFFFFLW\SLTLVAR

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						LECRAGVQWCDLGS LQPLPPQ\FE* FSCLSLQLALPRPAKFFV\LVEM\GF TMLAKMVSIS*PCDPPALASQSARIT ILDFMLAPACPLLIIPFTWTLFFRNTI
3013	8510	A	3272	3	367	
3014	8511	A	3273	58	553	VARSAPPDGAVCAGPGSRRTMAE QSDEAV\KY\YTLERFQMHN\HSKST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\ATENFEDVG\HSTDAR EMSKTFIIG\ELHPVDRPKLNKASGT FKGCV*GNFLFTTI*FLVPSWWTNW \VIP\AISAVGRRLGCIRL
3015	8512	A	3274	41	400	KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK\GEPLSSSSSSSPQK RGFPSSPEK\APGVPPPTPKGPSPPGG GVKKKGRA*KKKPLGLWEKGPNPA PGGPGTPTFGGPPGQYPG
3016	8513	A	3275	3	146	WGVITMMVTCSV/A/CTFLWLIAIL AQCNP LYRP*LKDETTWY LKHHWP
3017	8514	A	3276	161	472	
3018	8515	A	3277	3	273	AAAPGN GRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP\P SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAGCAEYQAPGL
3019	8516	A	3278	124	672	FQRTKLLNGPGDVETGTSITVPQKK WLHVISPFI VQSLTLPFLAKWGDRL QLLQIELAAREVSDI*EETV*NETYL LLLCSRKTLDTLKWAHSIPSYARLF YI**FSCSLKLAFSQFLPADPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFISPD S GF
3020	8517	A	3279	2	991	AAAAPGN GRASAPRLLLLFLVPLL WAPAAVRAGP\DEDLSHRNKEPPAP \PSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQT\NLGIYPMQF VAIIQLLIVSEIGVSRTFFIAAIMA MRYNRPGPCWAGAMLCL/AGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLK\MSPDEGQEE LEEVQAE LKKKDEEFQRTK\LLNG\ PGDVETGTSITVP\QKKW\LHFISPIF GQALTLTFLAEWGDRS*\LTTIVLAA REDPYGVA VGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP
3021	8518	A	3280	1	278	QHDLDQVDVAFTEEE*RLAGPAQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERN DQLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS
3022	8519	A	3281	263	588	DSALPQKEELKMNMFKEAVTFKDV AVAFTEEEELG\LLGPAQRKLYRDVM VEN\FRN\LLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLS\VK AL\LLYDLAQT
3023	8520	A	3282	1	1285	MEDSELPSARSVLPSKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT

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						QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLLENLRRKEEAEQLRRQK VEEDKRRRLLEEVLKREERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEEKAKKKAAAK KMEEVEARRKQEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHAWSQCLP*RLL\
3024	8521	A	3283	3	262	RVLRELQEREKALRLQKEQLQRELE EKKKKKEEQQLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IHHQYYQPPNLELFGTILPLDLEDIF KKSKPRYHKRTSSAVWNSPPLQGA RVPSSLAYSLLKKH
						FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVSC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE
3025	8522	A	3284	1	269	FFFFPQIGSHPTARLECSDAITFCCSL NLPGRDPPASAS*VAETTGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM
3026	8523	A	3285	3	1191	KSCFNAFFNFEDMQEITQH\FAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTSLSLKSIIGIVGAG AYIL\SRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSGLTTNVV\ EILAHHFGQEELQANLDLIQTYRM HIAQDINQDNLQFLNSYNGRRDLE IERPILGQNDNKSSTLKVVG DNPAVEAVMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVSTASAMTRLARSRTHSTSSSLG SGESPFSSVTSNQSDGTQESCESPD VLDRHQTMEISLDDVLLSALLRNN GKSAQKKISAKPKLEFLCPRPGTC DHGSRKFCYTVLVDPRESKATAV ALGSFPAGGPAELSLRLGEPLTIVSE
3027	8524	A	3286	3	638	SSKLSGLTTNVVDIILAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQFL L\KSYNGRRDLEIERPILGQNDNKS TLKG\STLLVVDNPAVEAVVECN SRLNPINTTL\KLMADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS T\SGSMTSVARSR\THSTSSSLGSGES PFSSVTSNQSDGTQESCESPDVL DRQQTMEVSC
3028	8525	A	3287	1	407	FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCLSLNSWDYRPAPP/* PG*LFFVFLVETGF/IHVGQPLKLL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFPTELML
3029	8526	C	3288	157	468	MHHIHNASRTFQLIFSSFPRGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQPFCTSPAACGQNLPIKHGL

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						PRWSTKGETTADTDSVDLENPILYK YFQL*
3030	8527	A	3289	14	348	EFHSCRPGWSAMTQSRLTLQPPPPG FK*FSCLSLLSSWDYRHTPPHPASF* LLVDTG\FLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSRL
3031	8528	A	3290	1	2201	MTNLAMVERDSEAGTAASRFPNGH AAKGKAQAHYKVWRPAEVRCLKL GPEWVTLRYTIKHPYKLCGKRQH VFFFTSRSDVGFMLTTLPFGSVSV ESKMNNKAGSFFWNLRQFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDDELKKNLNHE VSNEDVLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFFSSNYFTAM WTIAKRLSDDQKRFEKRLMFSPAF NQLCEHMMREAKIMQYKYLFLSLH AIVKLGIPQNTILVQTLLRVQTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVVDNIHGCPLRIMINILQ SCKDLQYHNLDLDFKGLADYVAATF DIWKFRKVLFILILFENLGFRPVGLM DLFMKRIVEDPESLNMKNILSILHTY SSLNHVYKQCQNEQFVEVMASALT GYLHTISS\ENLLDAVYSFCLMNYFP LAPFNQLLQKDISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL PQLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRM/D TNR\NQVLPL/SLDVGTTSAT\DIQRL LTYISFAGLSELKS
3032	8529	A	3291	3	485	LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSSHTNAKGGQRS*AALLGG EGTTPPSKD\HLAPHNYHIDFEIQN GTPNRNPSAYPLS\DVDTTSCLOQIFK E*LCYVFPRSAAYCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT
3033	8530	A	3292	1	530	LRKTFIPNRPLILLPPGNSLATHLFF\ ETVSRVAQAGVQWHHLGLLQSPS PGFKRFSCLSLPSNWDYRHAPPRLA NFIYFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVSFLLPYTHASSLLQ LLLAPLVTNGQGQEQKPELVREVG
3034	8531	A	3293	115	463	VTQQLFNILSFIFFHTSILIFFFFLKME SCSVA\RLECSGT\LAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**EQGFHHVGQAGLRTPGPQGD PARPWAPKVLGLQA
3035	8532	A	3294	503	1055	DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP

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						SNKTTWLRPLTQQF*NLPQKKT LA KK*KDFTHRVLFTA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLK WLLWRTGVS GGSETEIDSEVISGL
3036	8533	A	3295	3	304	FFLVETEFCHAAQAGVQWCDLGSL QPPPPGLQSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKPPF
3037	8534	A	3296	324	650	KKEHRVTCFSFWEMESRSVA*AEV Q*HDLDLQPLPHGLKRVSLSLPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWS\RTPDLVILPALAPQSAGITGG EPPCPATK
3038	8535	A	3297	2	564	FFFFPPQPPSPGFKQFSCLTLPSSWD YRCPPRPANF*FLIETGF/VHVGQA GLELLTSGDLPTPASQNA GITGVRP GTQPASCF*MWQGLIGQNKMTISLL LQSILL
3039	8536	A	3298	352	392	
3040	8537	A	3299	20	200	FTLIQNCFHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGNM VKPHLSLKF
3041	8538	A	3300	971	9082	
3042	8539	A	3301	1	15447	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES EH KNNNYEPNLFKTPQRKPSYNQ LAST PIIFKEQGLTPLYQSPVKEL DKFKL DLGRNVPNSRHKSLRTV KTKMDQA DDVSCPLLNSCLSESP VVLOCTHVT PQRDKSVVCGSLF HTPKFVKGRQTP KHISESLGAEV DPDMSWSSSLATPP TSSSTVLIV RNEEASETVFPHDTTAN VKSYFS NHDESLKKNDRFIASVTDSENTN QREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKV RTS KTRKKIFHEANADECEKSKN QVKE KYSFVSEVEPNDDPLDSN VAHQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEK IPLHHISSCDQNISEK DLLDTEN KRKKDFTLSENSLPRIS SL PKSEKPLNEETV VVKRDEEQHLESH TDCILAVK QAISGTSPVASSFQGIKK SIFRIRESPKETFNASFS GHMTDPNF KKETEASESG LEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSV ALKNAGLI STLKKKT NKFYAIHDETSYKGGKIP KDQKSELINCSAQFEANA FEAPLTF ANADSGLLHSS VKRSCSQNDSEPT LSLTSS FGTILRKCSRNETCSNNT VIS QLDYKEAKCNKEKL QLFITPEADS LSRKTSV SQTSLLAKKWLREGIFD GQPERINTADYVGNYLY ENNSNSTI AENDKNHLSEK QDTYLSNSSMSNS YSYHSDEVYNDSGYLSK NKLDSGIE PVLKNVEDQK NTSFSKVISNVKDA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPFAFRIAS GKIRLCSHETIKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVF DIQSEEILQHNQNMMSGLEKVS KISPCDVSLETSDICKCSIGKLHKS VSSANTCGIFSTASGKSVQVSDAS LQNAQVFSIEDSTKQVFSKVLFS SNEHSDQLTREENTAIRTPEHLIS QKGFSYNVNSSFSGFSTASGKQV SILESSLHKVKGVL EEFDLIRTEH SLHYSPTSRQNVSKILPRVDKRN PEHCNVSEMEKTCSEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQD KQQLVLGTVSLVENIHVLGKEQAS PKNVKMEIGKTETFS DVPVKTNIE VCSTYSKDSENYFETE AVEIAKAF MEDDELTD SKLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILV GEPSIKRNLLNEFDRIENQEKS LKASKSTPDGTIKDRRLFMHVS LEPITCVPFRRTKERQEIQNP NFTAPGQEFLSKSHLYEHLTLEK SSSNLAVSGHPFYQVSATRNEK MRHLITTGRPTKV FVPPFKTKS HFRVEQCVRNINLEENRQKQNI DGHGSDDSKNKINDNEIHQFNK NNSNQAAAVTFTKCEEEPLDLIT SLQNARDIQDMRIKKQRQRF PQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSK HCIKINSKNAESFQFHTEYFGK ESLWTGKGIQLADGGWLIPSN DGKAGKEEFYRALCDTPGVDPK LISRIWVYNHYRWIIWKLAAME CAFPKEFANRCLSPERVLLQL KYRYDTEIDRSRRSAIKKIME RDDTAAKTLVLCVSDIISLSAN ISETSSNKTSSADTQKVAIIE LTDGWYAVKAQLDPLLAVLKN GRLTVGQKIILHGAELVGSPD ACTPLEAPESLMLKISANSTR PARWYTKLGFFPDPRPFPL PLSSLFSDGGNVGCVDVIIQRA YPIQRMEKTSSGLYIFRNERE EEKEAAKYVEAQQKRLEALFT KIQEEFEEHEENTTKPYLPSR ALTRQQVRAIQDGAELYEAVK NAADPAYLEGYFSEEQLRALN NHRQMLNDKKQAQIQLEIRKA MESAEQKEQGLSRDVTTVWKL RIVSYSKKEKDSVILSIWRPSS DLYSLTEGKRYRIYHLATSKS KSKSERANMPAGRTV*K*SKKQ KSFYKRRGLGCSMSPSTTFKSG IQ*Y*LSIPEKSFI*S*KCQHS YFNSYFQGCSVKPSHDF*RQR IIQNVRQAQR*QL*I*C*INQK YSHGKESRCMCFK*KL*KR*AV AT*KIHESSITFKKGTINQNTN LRVIQKNQEE TTSISKITVNP DSEELFSDNENNFFVQVANERN NLALGNTKELHETDLTCVNEP IFKNSTMVLYGDTGDKQATQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSIKKDLVYVLAENKNSVKQHIK MTLGQDLKSDISLNIDKIPEKNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTTSEECRDADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDCKNSASGYLTDENEVGF RGFYSAHGTKLVNSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNDKTVSEKNNKCQ LILQNNIEMTTGTFVEEITENYKRNT ENEDNKYTAASRNSHNLEFDGSDSS KNDTVCIHKDETDLLFTDQHNICLK LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMSGLEKVSIS PCDVSLTSDICKCSIGKLHKSVSSA NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIRTPEHLISQKGFSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCNVSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTD SKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMMHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR

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						PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQONIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDBGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIIELTDG WYAVKAQLDPPLLAVLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPD RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVLSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSDEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVSASP KEGHFQETFNKMKNVTENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPPVSPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3043	8540	A	3302	1	2163	
3044	8541	A	3303	1	5771	
3045	8542	A	3304	1	3395	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRKTNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP

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						FESGSDKISKEVVPSLACEWSQTLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLWDF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTFRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC**E KPRALCKLRNGKNLQ*RI*IIK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQSLTC*EHSCFGKRTGFT*KRK NGNW*N*NFF*CSKENKYRSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNGFVKF KNWKKKRRAPYLSGRTL NQKKLIK *I*QDNRKSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLCTLSHN*GT SRDTESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFRSTSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LGGKQTKAKH*WTWL****

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						K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTFRFNYKSSECQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSRRPSSLCVFS*TAVYVWRF*T LHKN*QKCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRIL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKKDNGKG*HCKNTCSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVVC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIIAFQ*WRKCWLC*CNYS KSIPYTVDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNKTIFTITCTNKTASSCFARWC RAL*SSEECSRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLKF KRKRFSYTEYLASIIRFIFSVNRRKEI QNLSSCNFKI*K*I*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRICRFCCEKN RTCPFRLFVRRMLQFTGNKVLDRP* *GHY*ASYVNCCCKQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQQN EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPIS LNWFEELSSEAPPYNSEPAEESCHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTPLYQSPVKELDKFKLD LGRNVPNRHKSLRTVKTMDQAD DVSCPLLNSCLSESPVVLQCTHVTP QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMSWSSSLATPP TSSSTVLIVRNEEASETVFPHTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF R
3046	8543	A	3305	1	5771	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVD PDMSWSSSLATPP TLSTVLIVRNEEASETVFPHDTTAN VKS YFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSM PNVL EDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPN DTDPLDSNVAHQKP FESGSDKISKEV VPSLACEWSQLTSL GLNGAQMEKIPLLHISCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETV VNKRD EEQHLESH TDCILAVKQAISGTPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATT TQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKNSVKQHIKMTLGQDLKSDISLNI DKIEPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWWALLMPVHLLKPQN LLC*RFLLTVLGLLAGIPNLDSTLTL DLFLCPYHRFSVMEEMLVVLM*LF KEHTLYSGWRRHHLDTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNMCKTQQNHYYHHVH*QD SKFVLCKMVQSFMKQ*RMQQTQLT LRVISVKSS*EP*ITGKC*MIRNKLR SSWKLGRPWNLLNKRNVYQGMS QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDLPLSSICQ TNVTIYWQ*SFG*TLMTLLSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTSLCIYCMQMIPSGPPQLKT VLQGRDLLKSFLVQETSF*CLLLIVR YIIKVLVYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNSMKFLFWKVIQ*LTKNLH**IP KLFCLVQQEKNNLVSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQLKNIS
3047	8544	B	3306	16	10899	MPNVLEDEVYETVVDTSSEDSFSLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGNGAQME KIPLHHISSCDQNISEKDLLDTENKR KKDFTLSENSLPRISLPKSEKPLNE ETVVNKRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIRESP KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDQKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGILRKCSRNETCSNNTVISQDLDY KEAKCNKEKLQLFITPEADSLSCLQ EGQCENDPKSKKVSDIKEEVLA CHPVQHSKVEYSDTDFQSQKSLLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DHENASTLILTPTSKDVLSNLVMISR GKESYKMSDKLKGNNYESDVLT NIPMEKNQDVCALNENYKNVELLP PEKYM RVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSSEELFSDN ENN FVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLYGDTGD KQATQVSIKKDLVYVLAEEKNSV KQHIKMTLGQDLKSDISLNIDKIEK NNDYMNKWAGLLGPISNHSFGGSF RTASNKEIKLSEHNIKKSKMFFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPQKEQI TELSTILED SG SQFEFTQFRKPSYILQ KSTFEVPENQMTILKTTSEECRADAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTDEN EVGFRGFYSAHGTKLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVS MF KIENHNDKT VSEKN NKCQLILQNNIEMTTGT FVEEITENY KRNTENEDNKYTAASRNSHNLEFD GSDSSKNDTVCIHKDETDL LFTDQH NICLKLSGQFMKEGNTQIKEDLSDL TFLEVAKAQEA CHGNTSNKEQLTA TKTEQNIKDFETS DTFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVP SLACEWSQLTLS GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETV VNKRD EEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSSGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSMTFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNLCKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLSNELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDLELACETIEITAAPK CKEMQNSLNNDKNLVSIIETVPPKL LSDNLCRQTENLKTSSIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTSCSRKTSVSQTSLEAK KWLREGIFDGQPERINTADYVGNY LYENNSNSTIAENDKNHLSEKQDTY LSNSSMSNSYSYHSDEVYNDSGYLS KNKLDGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMGLEK VSKISPCDVSLETSDICKCSIGKLHK SVSSANTCGIFSTASGKSVQVSDAS LQNAQVVFSEIEDSTKQVFSKVLFK SNEHSDQLTREENTAIRTPEHLISQK GFSYNVNVNSAFSGFSTASGKQVSI LESSLHKVKGVLLEFDLIRTEHSLH YSPTSRQNVSKILPRVDKRNPEHCV NSEMEKTCSKEFKLSNNLNVEGGSS ENNHSIKVSPYLSQFQQDKQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFSDDVPVKTNIEVCSTYSKD SENYFETEAVEIAKAFMEDDELTD KLP SHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEPISIKRNLLNEFDR IENQEKS LKASKSTPDGTIKDRRLF VHHVSLEPITCVPFRTTKERQEIQNP NFTAPGQEF LSKSHLYEHLTLEKSSS NLAVSGHPFYQVSGNKGKMRKLI TTGRPTKVFPVPFKTKSHFHRVEQC VRNINLEGNRQKQNI DGHGSDDSK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKINDNEIHQFNKNNSNQAAA VTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRVFPQPGSLYLAKTSTLPRI SLKAAVGGQVPSACSHKQLYTYGV SKHCKIKNSKNAESFQFHTEDYFX*
3048	8545	A	3307	1	12500	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPPLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGLLAC*KMTVTKV LLVI*QMKMKWGLGAFILLMAQN* MFLKLCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YKILK*LLALL LKKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNLYLASL*RRETLRLKKI CQI*LFWKLRLKKHVMVILQIKNS *LLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWTF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPNVM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFMLMKSKVLVKSPVLAI NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKKCRILSIMIKTLFLLRLWCH LSS*VIYVDKLKISKHQKVVSF*KLK YMKM*KKKQKQVLQVLVTQISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKIISPKNKILI*V TVACLTAIPTILMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKS FV FHMKQLKK*KTYLQT VSVK*LRKTTRINQKFAKRKLWQV VTRHWMIQRIFFITL*IMMNVARIHI RFLTFRVKKFYNITKICLDWRKFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPHYCL KVTNIQTSSQEKILLYVLQNI*YPK KAFHIMW*IHLLSLDLVQQVESKFP F*KVPYTKLREC*RNLI*SELSIVFTI HLRLDKMYQKYFLVLIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNSWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAQ*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLICMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRIFTLNL SVLGILTWKRTDKSKTMDMALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPEIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFYAIHDE TSYKGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSRN ETCNNNTVISQDL DYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQKSLLYDHENASTLILT PTSKDVLSNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYMVRVAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAENKNSVKQHIKMTLG QDLKSDISLNIDKIPEKNNDYMDKW AGLLGPISNHSFGGSFRASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPQSINTVS AHLQSSVVVSDCKNSHITPQMLFSK QDFNSNHNLTSPQKAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRDADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KNDCNKSASGYLTDENEVGFRGFY SAHGTKLNVSTEALQKAVKLFSDIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNNKCQLILQ NNIEMTTGTFVEEITENYKRNTENE DNKYTAASRNSHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNICLKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKIVNFFDQKPEELHNFSLSNSELHS DIRKNKMDILSYEETDIVKHKILKES VPGVTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNDKNLVSIVTVVPPKLLSD NLCRQTENLKTSSKIFLVKVVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPAP RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNIHSASN LSESSSRPSSLCVFS*TAVYVWRF* TLHKN*QKCRVFSVS/TLKILVRK VYGLEKEYSWLMVDGSYPMMER LEKKNFIGLCVTLQVWQSLFLEFGF IITIDGSYGNWQLWNVPFLRNLLID A*AQKGCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKLVVQIPKKWPLLN LQMGGMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWWALLMPVHLL KPQNLLC*RFLTTLVGLLAGIPNLD FLTDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHHLDTYFA MKERKKRKQQNMWRPNKRD*KPY SLKFRRLKNMKKTQQNHYYHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNLKELTYS*QRQKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQTF SHLVLRWT**DLSFLL*KKQDLPLSS ICQTNVTIYWQ*SFG*TLMRTLLSLI C*LLQATSSGDQNPNAFLLYLLEIF LCFLLVQKRATFKRHSTK*KILLRIL TYFAMKQKTSLSICIYCMQMPSPGPQ LKTVLQGRITLLKSFLVQETSF*CLLL IVRYIHKVLYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFSHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQQEKNNLYLSVNPLGL LPPVQKIISD*NDVVHL*SKNRRVP RPVRKNVRKISRTQLQLKNIS
3049	8546	A	3308	1	9344	
3050	8547	A	3309	1	18345	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPDHTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPPLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDDTFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSFMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITDACRKDSVKMIQKAKKFQI*KK RSWLQHVTVYNIQKWNTVILTFNP RKVFYMMKMPALLF*LLLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIKMYVL*MKIHK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLK NFSQTMRIILSSK*LMKGILL*EILR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NFMKQT*LV*TNPFSRTLPLWFYMET QVINKQPKCQLKKIWMFLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TNGQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IIKRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTH*HLAKRQKLQNFLLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNLKVQLKLNGSLA C*KMTVTKVLLVI*QMKMKWGLG AFILLMAQN*MFLCLKCKKL*NCLV ILRILVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKIINAN*YK IILK*LLALLKKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFVF IKMKRTCYLLISTTYVLNYLASL*R RETLRLKKICQI*FWKLRKLKKHV MVILQIKNS*LLKRSKI*KILRLLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWTF*V MRKQT*LNTKY*KKVSQLVLEIN** PSRDNPVNMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFLMKKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIYVDKLKISKHQ KVSF*KLKYMKM*KKKQQKVLQL VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQKNGLEKEYLMVNQKE *ILQIM*EHCMIHQTVL*LKMTKIIS PKNKILI*VTVACLTAPTILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTHKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLIVI ILR*GHLHLG*PVVKSFFVHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIRFLLTFRVKKFYNITKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKKILLYVL QNI*YPKKAFFHIMW*IHLLSLDLKL QEKY*K*R*QIYCCO*KFS*LRI*WQ *FK*K*YCLYS*R*NGLAII*SAQHM S*IIWPVYEGGKHSD*RRFVRFNFFG SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETTRIA*LFLKF*ITF* HKKEQNGHSLK*GNRHS*TQNLKE SVPVGTGNQLVTFQGGQPERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPCKKE MQNSLNNDKNLVSIEIVVPPKLLSD NLCRQTENLKTSSKIFLVKVHENV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDITYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPAPF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMMSGLEKVSIS PCDVSLETSICKCSIGKLHKSVS NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSKNEHS DQLTREENTAIRTPEHLISQKGFSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTS QNVSKILPRVDKRNPEHCNVSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLGTKVSL VENIHVLGKEQASPKNVKMEIGKTE TFSVDPVKTNIEVCSTYSKDSSENYF ETEAVEIAKAFMEDDELTDKLP ATHSLFTCPENEEMVLSNSRIGKR GEPLILVGEPKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNFTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFPVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNIN DNEIHQFNKNNSNQAAAVTFKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIWKLAAMECAFPKEFANRCL SPERVLLQLKYRSTASGKQVSILESS LHKVKGVLEEFDLIRTEHSLHYSPT SRQNVSKILPRVDKRNPEHCNVSEM EKTCSEFKLSNNLNVEGGSSENNHS SIKVSPYLSQFQQDKQQLVLGTKVS LVENIHVLGKEQASPKNVKMEIGKT ETFSVDPVKTNIEVCSTYSKDSSENY FETEAVEIAKAFMEDDELTDKLP HATHSLFTCPENEEMVLSNSRIGKR RGEPLILVGEPKRNLLNEFDRIEN QEKSLKASKSTPDGTIKDRRLFMHH VSLEPITCVPFRTTKERQEIQNPNFTA APQEFLSKSHLYEHLTLEKSSSNLA AVSGHPFYQVSATRNEKMRHLITT GRPTKVFPVPPFKTKSHFHRVEQCVR NINLEENRQKQNIIDGHGSDDSKNIN DNEIHQFNKNNSNQAAAVTFKCE EEPLDLITSLQNARDIQDMRIKKK

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						QRQRVFPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTA AKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAIIELTD GWYAVKAQLDPPLLAVLKNGRLT VGQKILHGAELVGSPDACTPLEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQQRLEALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAAIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVILSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTQYQQLPVSEIL FQIYQPREPLHFSKFLDPDFQPSCE VDLIGFVVSVVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFS VFS ASPKEGHFQETFNKMKNTVENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRA LDFLSRLPLPPPVSPICTFVSPAAQK AFQPPRSCGTKYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRTAP TSSDYRLRKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI
3051	8548	A	3310	1	7988	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESLH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNRSHKSLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKS VVCGSLFHTPKFVKGRTQ KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPDHTTAN VKSYFSNHDESLLKNDRFIASVTD ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRITKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSVPVQSGIKK SIFRIRESPKETFNASFGHMTDPNF

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						KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPRK VQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKND CNKSASG YLT DENEVGFRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSV VSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEA CHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVSI ETVVPKLLSDNLCRQTENLKT SKSI FLKVKVHENVETAKSPATCYTN QSPYSVIENSALAFYTSCS*KSONIK KYL FES*ST*KCRKRNSKKSCNLLH KSVPLFSH*KFSLSLHLKL*RKTSVS QTSLL EAKKW LREGIFDGQPERINT ADYVGNYLYENNSNSTIAENDKNH LSEKQDTYLSNSSMSNSYSYHSDEV YNDSGYLSKNKLD SGIEPVLKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKNKNAAIKLSI SNSNNFEVGPPAFRIASGKIVCVSHE TIKKVKDIFTDSFSKVIKENNENSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEEILQHN

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						QNMMSGLEKVSISKISPCDVSLETSIDIC KCSIGKHLKSVSSANTCGIFSTASGK SVQVSDASLQNAQVFSEIEDSTKQ VFSKVLFKSNEHSDQLTREENTAIR TPEHLISQKGFSYNVNVSSAFSGFST ASGKQVSILESSLHKVKGVLEEFDLI RTEHSLHYSPTSQRQNVSKILPRVDK RNPEHCVNSEMEKTCSEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLGTKVSLVENIHVLGKEQA SPKNVKMEIGKTETFSQVVKTNIE VCSTYSKDSSENYFETEAVEIAKAFM EDDELTDKLP SHATHSLFTCPENE EMVLSNSRIGKRRGEPLILVGESIK RNLLNEFDRIENQEKSLKASKSTPD GTIKDRRLFVHHVSLEPITCVPFRRT KERQEIQNPNTAPGQEFLSKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLITGRPTKVFVPPFKTK SHFHRVEQCVRNINLEGNRQKQKQID GHGSDDSKNKINDNEIHQFNKNNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKKQQRQVFPQPGSLYL AKTSTLPRISLKAAVGGQVPSACSH KQLYTYGVSKHCIKINSKNAESFQF HTEDYFGKESLWTGKGIQLADGGW LIPSDGKAGKEEFYRALCDVKAT
3052	8549	A	3311	1	14305	MPIGSKERPTFFEIFKTRCNKADLGP ISLWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSIDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV

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						MISRGKESYKMSDKLKGNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSMMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEAHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVS ETVVPKLLSDNLCRQTENLKTSKSI FLKVKVHENVEKETAKSPATCYTN QSPYSVIENSALAFYTSCSRKTSVSQ TSLLEAKKWLREGIFDGQPERINTA DYVGNYLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLDGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFTDSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKVFADIQSEEILQHNQ NMSGLEKVSKISPCDVSLETSDICKC SIGKLHKSVSANTCGIFSTASGKSV QVSDASLQNAQVFSEIEDSTKQVF SKVLFKSNEHSDQLTREENTAIRTP HLISQKGFSYNVNVSSAFSGFSTAS GKQVSILESSLHKVKGVLEEFDLIRT EHSLSHYSPTSQRQNVSKILPRVDKRN PEHCNVSEMEKTCSEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQDK QQLVLGTVSLVENIHVLGKEQASP KNVKMEIGKTETFSQVVKTNIEVC STYSKDSSENYFETEAIVEIAKAFMED

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						DELTDSKLPSHA THSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSIKRN LLNEFDRIENQEKS LKASKSTPDGT IKDRRLFMHHVSLEPITCVPFRTTKE RQEIQNPNTAPGQEFLSKSHLYEH LTLEKSSSNLAVSGHPFYQVSATRN EKMRLHITTGRPTKVFVPPFKTKSH FHRVEQCVRNINLEENRQKQNIDGH GSDDSKNKINDNEIHQFNKNNSNQ AA AVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQRQRVFPQPGSLYLAK TSTLPRISLKAAVGGQVPSACSHKQ LYTYGVSKHCIKINSKNAESFQFH/T *RLF*WKFM DWKRN TVG*WWM AHTLQ*WKGWKRRIL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETLRLKKICQI*LFW KLRKLKKHVMVILQIKNS*LLKRS KI*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLIRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPVMKRSKNLL CWVFIQLAGKKLKLQRLWTK*KT FLMKKSKVLVKSPVLAINGQRP*ST ERPVKTLN*HVRPLRSQLPQSVKKC RILSIMIKTLFLLRLWCHLSS*VIHYV DKLKISKHQKVSF*KLKYM KM*KK KQKVLQLVTQISPLIQSLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EIICMKIIQT VL*LKMTKIISPKNKILI*VTVACLT APTILMRYIMI QDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFHMKQLKK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQVVTRHW MIQRIFFITL*IMMNVARIHIFLLTF RVKKFYNITKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEKKILLYVLQNI*YPKKA FHIM W*IHL LSLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSENNHSI KVSPYLSQFQQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFS DVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDEL TSKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFPVPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEYDFGKESLW TGKGIQLADGGWLIPSDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIIEITDG WYAVKAQLDPPLLA VLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRLAQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSDEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASN QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKRRALDF LSRLPLPPPVSPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3053	8550	A	3312	11089	17637	NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHKILKESVPVGT GNQLVTFQGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVKNLDFE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVSIVTVVPPKLLSDNLCRQ TENLKTSSIFLKVKVHENVKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLEAKKWLREGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDITYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDGIE PVLKNVEDQKNTSFSKVISNVKDA

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						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDEILFQIY QPREPLHFSKFLDPDFQPSCEVDLI GFVVSVVKKTVRNEEASETVPFHD TTANVKSYSFNHDESLKKNDRFIAS VTDSSENTNQREAASHGFGKTSNGNSF KVNSCKDHIGKSMNPVLEDEVYET VVDTSEEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVP SLACEWSQ LTL SGLNGAQMEKIPLLHISSCDQNI SEKDLLDTENKRKKDFLTSENSLPRI \SSLPNPEEPLNEETVVNKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEASESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEAF PLTFANADSGLLHSSVKRSCSQNDS EPTLSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSLSCLQEGQCENDPKSKKVSD IKEEVLAACHPVQHSKVEYS DTF QSQKSLLYDHENASTLILTPTSKDV LSNLVMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYM RVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENN FVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVL YGDTGDKQATQVSIKKDLVY VLA EENKNSVKQHIKMTLGQDLKS DISLNIDKIPEKNNDYMNKWAGLL GPISNHSFGGSFRTASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVSDCKNSHITPQMLFSKQDFNS NHNLTSPSQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKTTSEECRDADLHVIMNAPSIGQV DSSKQFEGTVEIKRKFA GLLKND CN KSASGYLTDENEVGRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVS MFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEACHGN TSNKEQLTATKTEQNIKDFETS DTF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLNSELHSDIRKNKMDILS YEETDIVKHKILKESVPVGTGNQLV TFQGQPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNLDFEKEQGT SEITSFSHQWAKTLKYREACKDLEL

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						ACETIEITAAPKCKEMQNSLNNDKN LVSietVVPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLLEAKKWREGIFDGQPE RINTADYVGNYLYENNSNSTIAEND KNHLSEKQDTYLSNSSMSNSYSYHS DEVYNDSGYLSKNKLDSGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAAI KLSISNSNNFEVGPAPFRIASGKIVC VSHETIKKVKDIFTDSFSKVIKENNE NKS KICQTKIMAGCYEALDDSEDIL HNSLDNDECSTHSHKVFADIQSEEIL QHNQNMSGLEKVS KISPCDV SLETS DICKCSIGKLHKS VSSANTCGIFSTA SGKSVQVSDASLQNAQVFSEIEDS TKQVFSKVLFSNEHSDQLTREENT AIRTPHEHLISQKGFSYNVVNSSAFSG FSTASGKQVSILESSLHKVKGVLEEF DLIRTEHSLHYSPTSRQNVSKILPRV DKRNPEHCVNSEMEKTCSEFKLS NNLNVEGGSENHNSIKVSPYLSQF QQDKQQLVLGTVSLVENIHVLGK EQASPKNVKMEIGKTETFS DVPVKT NIEVCSTYSKDSENYFETEAVEIAK AFMEDDELTD SKLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLNNEFDRIENQE KSLKASKS TPDGTIKDRRLFMHHVSLEPITCVPF RTTKERQEIQNPNTAPGQEF LSKS HLYEHLTLEKSSSNLAVSGHPFYQV SATRNEKMRHLITGRPTKVFPVPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAAVTFTKCEEEPLDLITSL QNARDIQDMRIKKKQRQRFVPQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHKIKINSKNAE SFQFHTE DYFGKESLWTGKGIQLAD GGWLIPSN DGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSANJSETSSNKTS SADTQKVAIHETD GWYAVKAQLD PLAS
3054	8551	A	3313	1	207	CNLC L P D S S D S P A S A S Q V A G K T G L C H H T G V V F V F L V E M G F H H A G Q A G L E L L T * V I C V P Q P P K A L G L Q V
3055	8552	A	3314	279	625	S L Y V C M H V C M Y V F I L R R S F A L V A Q A R V Q W C G L G S L Q P P P P G F K R F I S C L S L P T S * D Y R R A P P H P T N F F V F S A E M E F H R V S Q D G L Y L L T S G D L H P R L A S Q S A G I T G V S H R T R P F L L
3056	8553	A	3315	1	418	G S I P P P G V \ Y C V P Y P L K H A P A P A L P * T R Q R G S P Q S P G A L R A K * H V L L E T P Q P P G P A P P G A R T R T R P E S E * S Q P G R S P

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						VSRQSLTGADALEGPCLGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG
3057	8554	A	3316	1	354	GFIPPPGV\YCVPYPLKHAPALP* TRQRGSPQSPGALRAK*HVLLETPO PPGPAPPGARTRTRPESGAWRWVR AGSSPPPPSPHPTPPCFQVHQGLRS GSANEASLEDPQSRDRA
3058	8555	C	3317	299	365	MSCPECNLTGISSKTNKKLNQ*
3059	8556	A	3318	33	302	PSSWDYRHAPPRLTNF*\FLVEMGF HYVG/QAGLELLSSGDPPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHQNHGPRVVGQAKP
3060	8557	A	3319	3	409	SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGAIGK ARQAAKTEIEKLQMKEMTCRDIK EVAKIYIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
3061	8558	A	3320	1	255	
3062	8559	A	3321	1	395	FGYNIPLNHLDPDRVAMYVHAYTLY SAVRPFGCSFMLGSYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIKVEAKIYI VHDEVKDKAFELELSWVGE\ESLKE EDESDDDNM
3063	8560	A	3322	515	560	
3064	8561	A	3323	3	661	KDGVVLGVVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\VAG\LLADARSLA DIAREEASNFRSNFG\YTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GSYSVNDGAQLYMID\SGVSYGY WG\CAMRQAR\QLAKT\ELERLQLK KLPSGDIVKEVAKIYIVHDEVKDK AFELEL\SW\VGDLTK*\RHEILPKD\ LRDEAEKYAKESLKEEDESDDDNV
3065	8562	A	3324	3	634	
3066	8563	A	3325	2	487	HIFGKAKEYANSQVVTKDQYAVIC LGGDAVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKIVKPVHYD RVKKITQRKKEIPVFLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RRLLRFSITDRTQMGR
3067	8564	C	3326	373	727	MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCAPAQPAYLTHDVNS QVSLIKTSLQASSGSXXXXXXXXXX XXXXXXXXXXGAQAFFLGGGFF*
3068	8565	A	3327	2	536	VHLVPRQNACAIRLTECPRLK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GW\QTPDLRRSTRLSI PKCWDYRREPPHPVKIFLKLSSFSY WVFPVCALNLSLSLFVYTFLSNLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLSSHTKPCQFS HESA

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3069	8566	A	3328	3	334	FLRQGL/NSVTQAGVQWGDLSLQ PPPPKLGSSHPSPSSCRHYRHTPP/ RSG*FFVFL*RWGFAMLPRLV*TSG \PSDMPALASQGAGTTSMSHHTWR PYLNFQKFPKKN
3070	8567	A	3329	1	148	PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWNLNTHWISEN SGHCMVLMMLTVRSCS
3071	8568	A	3330	3	267	FFFFLRDRFSLCGPGWSAV/VQS*LT VNS/TFLGPSNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLPRPVLKSW PQAIFLRHAPKVLGVEV
3072	8569	A	3331	3	269	FETESHSVT\RLCSG/TILAHCNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVGGAGLELLT*VIC LPRPPIVLGLQA
3073	8570	A	3332	1	299	FSLIKISMMLLMKMEK*NLOFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLNS NINRHICSQILITKVPGANTKDHP
3074	8571	A	3333	3	261	RQDLSLCHPGWSAVVQS*LIALTS* \VKQSTYLRHPTSWG*RCVPPCPAN FCFFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV
3075	8572	A	3334	3	290	VDFFFFFFSRRSNVLSHRLECSGTISS HGNLCLLGSSDSPASASQVARITGV HHHTQLIFIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA
3076	8573	A	3335	3	358	
3077	8574	A	3336	76	386	VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPAAAAPHCPAPCA PRH*GSR*LESPAPQGPQSRAARMP AWPLPPAPPTDPTAPPAPRSHWPA PPT
3078	8575	A	3337	66	381	VLPPPSSPALHSPAPPSTCPYLPGAL PPLE/GPPSRPPRTFIGNPGGQGPGE VSPIVLRSPSQPH*PGNQGPCSSQP PGSPRSEHGC*HRCWALYGQKEP APS
3079	8576	A	3338	1	303	KDRFSFCGPG*SAVTQLNLTA DP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSW/PQ VILSPLSRARATAPSFPLFSSKDEPI
3080	8577	A	3339	2	212	RFSCSLPSSWDMHHSPG*FFIFLVE TGFAHVGQAGLELPASNDPPASTS QSVVITAMSHRRALVPIF
3081	8578	A	3340	2	273	RRSSTQPPRLQCSGTIPAHCNLHPPS PSDYPAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPPKVPGPQA
3082	8579	A	3341	135	494	IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIA CDCAFSMYDGLFCNSNS RADWSHCTVSGTYQHTENSIMS

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3083	8580	C	3342	71	217	MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA*
3084	8581	A	3343	1	106	
3085	8582	A	3344	2	1926	MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSTCRRLRELCQSSGKVV KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQQPDDYESYLE GAVYIDQYCNPLSDISLKDIQAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELQSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLIR RTGIPISMSLLYLTARQLGVPLEPV NFP SHFLLRWCQGAEGATL\DIFDYI YIDAFGKGKQLTVKECEYLIGQHVT AALYG\VVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLA\MY PDQVQLLLLQARVYF\HLG\ILPEKS FCLVLKVL DILQHIQTL\DPGQHGA VG\YL\VOHTLEHIL\ERKKEEVGVE VKL\RSDEK\HRD\CY\SFGFIMKA* RGMG\Y*LC*FYGW\DP TWHGSGHE LDSRNMNV\HSLPHGHHQPFYNVL VEDGSCRYA\AQEN\LEYNAEP\QEI SH\PDVGRVYSQRFT\RTHYIP\NAEL \EIRYPEDLEFV\YETVQ\NIYKCKRK ENIE
3086	8583	A	3345	59	339	
3087	8584	A	3346	1	342	FCSCQPQAGVQRRDLSSLQPLPP\GF K*FSCLSLPSSWD\YRRPPP/RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLLLN CLLPFLGIPLHSPL
3088	8585	A	3347	1	294	ETESHSVTRLECSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGQTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFSCLSLPNSWDHRCTPPHLA NFCIFCRDGFPPCWPDSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP
3089	8586	A	3348	2	268	EAESHVA\RLCSDAISAHCNLRLP GLSNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA
3090	8587	A	3349	3	444	FFFEIWSGSVA\RLCEGGTIFVAHCNL RLLGSSHPPTSAS*VAGTKGTCHHV QLIFAFFVDTGFHHVARLVLSN*TQ AICPPRPPKVLGSYASITAPGPTFFFL TIILGVQVDKRFYGNLTRKDIQKLG NYVWEGLELLSPQKFMLKP
3091	8588	A	3350	1	318	FFFFFLRQSFALAQAGM/QWHDLG LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL

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3092	8589	A	3351	16	848	VGSGLVSAQQTGCGPGNPSPPGSVS GAMELRVEPAARGQGS LGDPPA\VL LPGALELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPPVSPAPTGWDL VSQ LQPVSSPRGRCP RSGPDLLPLH GQPFHSSSFSSSMQASGE PVQPCPS RSSGS/VKGG LQTVEPE SGPGALKC EALAWLRG*GLLGHS GFAGSVPEV TPGSPHVLNP\GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSP TS*GIP*HRKPWVFSVMHKVG WKV
3093	8590	A	3352	1	293	VLRQGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL\NCIAQAGLE/PP GFK*/CPKHWDYRHEPGMPGWVFLI S
3094	8591	C	3353	127	345	MDFELELFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFLLKKL CF*
3095	8592	A	3354	2	215	AHCNLC L PGSSDSPASASRV TGITG VHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLRT
3096	8593	A	3355	164	311	QRSQGIWVWRFIRF*II
3097	8594	A	3356	1	381	YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAAFIIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIKNNE*LIHKTTWKNLKEARA SGV
3098	8595	A	3357	2	764	RTLHLFAGGCGGTVGAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRAVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSFQCQTARLVFREESYL PL
3099	8596	A	3358	155	875	DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRGS KQMNTLQCARYVY/HDRKAFGGFY RGLTASYAGISETIICFAIYESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGL\ASCMAYSHTEVH* GRR L\REKGHPSTKSFCPERRALGVP GEEGYPCLFIEGLFAPSFIRQIP\NTA\ IVLGYLWRLIVYLLGRP
3100	8597	A	3359	1	281	FFFAPETESYSVAIRLECSGTILVHCT LCLPGSSDSPASASQVAGTTGACHH TWLILVILVEIGFHHVQGAGLG/IS*L QVIRPPWAPKVLGIIG
3101	8598	A	3360	135	218	TLQFTSLISYSFCQSWGSKVPLSLPP

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						P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F
3102	8599	A	3361	198	390	
3103	8600	C	3362	5	316	MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXRLI YYRLLFSPCHSF*
3104	8601	C	3363	186	323	MPWLEHTAHFPDKAWITRMALLRN GIVPYDSLPLWITLGRWPNGGT*
3105	8602	A	3364	2	3096	TPRLQSNTRALYQYCPPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDLAWKKEVEKKPPM MSIDDAYEVLNLPQGGPHDESKIR KAYFRLAQKYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIIL ILKTQSILFNRHKEDLQPYKYAGYP MLIRTITMETSDDLFSKESPLLPAA TELAFHTVNCALNAEELRRENGLE VLQEAFCVAVLTRSSKPSDMSVQ VCGYISKCYSVAAQFECEKITEM PSIIKDLCRVLYFGKSIPRVAALGVE CVSSFAVDFWLQTHLFQAGILWYL LGFLFNLDYDTEESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEQHGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQV/AL* EVVNIVTSNQDCVNNIAESM/VLSSL LALLHSLPSSRSAWFWETLYALDIR VQKLIKEAMAKGALHLLDMFCNS THPQVRAQTAEFLAKMTADKLIGP KVRITLMKFLPSVFM/DAMRDNPE AAVHIFEGTHENPELIWNDNSRDK VSTTVREMMLEHFKNQDNPEAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLKPREFLIALLEKL TELLEKNNPHGETLETLTMTATVCLF SAQPQLADQVPPLGHLPLKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLEGGIGLENLADSPAAT*GS ELVKALQGQ*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHDLFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPVDHEAGDLGYQT
3106	8603	A	3365	1	358	NRLNATPIKIPTAFFAEMDKLNPFL KLNS*NLRYNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRH/DQ*NR NQSPEINP*YIGKLFSTVL

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3107	8604	A	3366	2	40	LPRLKQFS\CLSLPSSWDYKR\RP PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE*S AS
3108	8605	A	3367	1	223	IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCMKLEN IMLSERSQLQRATYCNDIAIYKNPE
3109	8606	A	3368	307	332	TTYHFFF*TESHSAQAQAHWRDLS SLRPPPPGFKPFSCLSWDYRRTPPH PANFLAFLADTGLHHAGQAGLKLL TSNDPPTPASQSAGTTGVSHRAQPF FSELPITIFFSL
3110	8607	A	3369	3	411	QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPQ* PFQGRFDAPPGYKQQTRPGHT/GQK GLRGPRQTLSLTSQPTACSENSQG SQPSPKRTLS
3111	8608	A	3370	3	166	EESCSVVQGGVQWCDLS*LQTLPP\ GSSNFCASASRVAGITGAHHHAQL KKKMLF
3112	8609	A	3371	4	312	FLR*SFTLIVQAGVQWRYLGSLQPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPSHRTWLRS FLI
3113	8610	A	3372	3	282	FFFETGSNSVAQAGVQWCNHSRLR PRPSG\SSDPPNSSSQVAWTTGVHH TQLLFKFFCKDEVSLCFPDWSQTV* RVEHIRDEYETTQHCLYPSN
3114	8611	A	3373	1	164	ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCPA TLLNT
3115	8612	A	3374	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3116	8613	A	3375	363	1246	DTEQIYCIQEPEYGGKKYCTKQSR YVSWTTHFSSSFIDQSLLESMA*KS TAPHSSDF*DFLT*KT*NLFFFLRRSL ALSPQAGVQWRDLGSLQAPPPGFTP FSC\PASPSSW\DYRHLPPCPANFFVF FLVETVSIFVFTVLAGMVSIS*PQ/CD PPTLASQSAGITRLSHRAR\LCFVF* KKRNAREGGRLLTIKADFLIFFSFF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRRPPQLA NF\CIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA
3117	8614	A	3376	3	324	DRISLCCPGWSAIV\QSQLTAA\SLPG LKQSFYISLPSS*GHRLAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN
3118	8615	A	3377	3	673	RWSHSVQAGVQWRDLSSRQPPVP GSRDSPASAS*VAGTTGTTHHAQFF FFFFLRRS/LSSV/SQDGVQWHDH SLQPVPPGFKQFSCLSLPSSWDYRC AAPRPANFFVF**RRVFSTLARL VSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCVHGQAGAVLILCLF LHSKINMFSPLHCTPASTV\YSHLPQ RPTKRRLYIRWRWERTWPANAEL
3119	8616	A	3378	2	323	RRSFTLVAQAGVRWHILGSLQPLPP GFKRFSCSLSPSGWDYRLMPPCPAN F*FLVEMRFHHVVGQAGPERLTSGD LPA*ASQSAGITGVTATPSQYKLCSL IIMKLN
3120	8617	A	3379	1	311	DFFF*ETASHSVTQAGVQWCDPSSL QPPPVFKQSSCLSLPSSWDYRHVP PCSVDT/CISILLIPFLRSGE*SPLLS WSSCDLGQGTAPLGFWPFMGKARP V
3121	8618	A	3380	3	404	PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHS\VAQAEVQWHDLGSL QPLTPRFKRFSCSLSPSRWDYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR
3122	8619	A	3381	739	1003	NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSLSLLSS WDCRHMPPNLA/NF/CVLRDKISPF CPGWSQTPGLKQCEIF
3123	8620	A	3383	1	299	ETESGSLPRLECSGTISAHCNLRLL GSSNSPVAS*VAGTGACSHAQLIF VFSVESGFRHVGGAGLNF*PQVIHP PRPRKVLGLLPVSHHTRPISFFL
3124	8621	A	3384	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH
3125	8622	A	3385	2	318	FLSSHLFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLSPSSWDYR RPPPRPANFFVFLVKTGF\TVLARM VSL*PHDPPASASQSAGITGVSHW CPANN
3126	8623	A	3386	1	325	ASTAQAGVQWPAAQLQTPPPGFTP FSCLSLPSSWDYRRPPSPANFLYF* *RRGFTMLARMVSI*PCDPPASSSQ SAGITGLSHRARPVIRILRRAGRNT IGGLD
3127	8624	A	3387	3	530	RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLSPSSWDYRRPPRPA /NFFVFLVET\GFTRGSIS*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLTSLCFLKLLTGEEAPMP/PF* RQS*CLTSVTLSA WRSICYDRLVDI QFKILFMKTKLPLFFSQNELYFIIL
3128	8625	A	3388	3732	4979	NFVFLYLRELSSQAKSLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFKHHVLY WLFGLVFLNLLLLILPVLYNEHRKIL

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						E*GRKVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHGQACSIKMIFLKDVNCA*LIGYI LFCFFFFFFFFLRCGVSSVAQAGVQ WRNLGSLAQAPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFLDF**RPL VFL/SFTVLARMGLNIS*PRDLPTSAS QSAGITGVSHHVQLPYFVLNKFTV LGSNSGF
3129	8626	A	3389	1	585	AAAAFLRQGLALV/THAGVQGQDYS SLQPLPPGLKAILLPQPPECWDYRC MSPCLA/N/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECVDLHILLICSHFYRL
3130	8627	A	3390	3	459	QPGVQWHDLSMQPPPRFKCFSC SLL/SS*DYRCPAPMPQPNFCIFI*RY GFT\MLASLVLDL*L*VIRPPWVSQS AGITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQPL*GS/WDP ET*HNGHFHFVWIKQSEPPIFKGRR*N P
3131	8628	A	3391	1	258	FFFKTDSCSVA\RLSEYGAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLLTLWIH CPPKMLGLQA
3132	8629	A	3392	3	316	VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPALASQS AGITGVHPPAPNSSCLHTDKRVHT WHKPS
3133	8630	B	3393	49	279	SSSDSDDEEKKHEKLKKALNAEEA RLLHVKETMQIDERKRPYNSMYET REPTEEEMEAYRMKRQRPDDPMAS FLGQ*
3134	8631	A	3394	2	357	
3135	8632	A	3395	1	1765	MSATTVVDAVNAAPLSGSKEMSLEE PKKMTREDWRKKKELEEQRKLG APAEVDEEGKDINPHIPQYISSVPW YIDPSKRPTLKHQRPPQEKQKQFSSS GEWYKRGVKENSIITKYRKGACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANSKPH QWGEENSPNSQTEKDHNSDEDEDK YADDIDMPGQNFDSKRRITVRNLRI REDIAKYLRNLDPNASAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGDITISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFVKKE DFKEQQKESILEKYGGQEHLDAPPA ELLQAQTEDYVEYSRHGTVIKQGER AVACSKYEEDVKIHNHHTIWGSYW KEGRRGN\KCCHSFSKYSYCTGEAG

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						KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEEKRRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E A\RLLVKETMQ\IDERKRPYNSMY *TSRP\IEEEMEAYRMKRQRPDDPM ASFLGQ
3136	8633	C	3396	106	426	MFLKEPVXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXRLXXXXG*
3137	8634	A	3397	25	435	TKYWLLFFLILPFFFWRRSRSVT QAGGQWHDLGSLQPPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVNSRSQ/CDPLASAS QSAGISGKSQHTRPVLVLLKTYTNS H/SF*VKGLGWEFIL
3138	8635	A	3398	3	320	KTESHSVTQAGAQQWDLSSVQSPP PGFKRFSCLSLPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAGITGVSHCARPIVIFL YLITSR
3139	8636	B	3399	70	199	XMQVTGFGRGQNHNVQGSTPTDAS PRRDVCTAQTQDSKLVNS*
3140	8637	A	3400	198	397	TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PPIACPAGTHPCGPYPC CHVGGGWPAQPLAALG
3141	8638	C	3401	164	313	MTLHFQELKSLKFYLNXXXXXXXXXX XGGRFKGSLGGPKFTRACNVKAFL L*
3142	8639	C	3402	165	361	MVKFCANNQKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGHLPGRV*
3143	8640	C	3403	146	389	MTPISLKGRCRQLGDGKRCSLEDLA LIEGCPHAGRPPPRKSTLEPAFGSPR CQDPVSAMCMTRSPANLDSAERQ APGLGR*
3144	8641	C	3404	157	404	MLSLTSSPLNQKGVVSFVHIAILKY QGCKPHFIKKLSRXXXXXXXXXXXXX XXKXXXXXXXXXXXXXXXXXXXXXP PAPSFLWEGE*
3145	8642	C	3405	73	252	MHTPLLAWPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP*
3146	8643	A	3406	2	617	IYIFLKALNFCREVVPISPPPKVRVLF KDSQVTSFPVPAL*KGGQGLGYKT APYKEKTNSLQARVNLGSPRGPLK RPPSSSSSPNPNALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAAWDP PAGCAQPPTVSPDPTKQVSRTKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPPVPDGNPV LN
3147	8644	C	3407	129	281	MSSHARVNLGPSKDPLKRPPXXXX XTQRQLFKTFINRCLQFVDFFEKIKL *
3148	8645	A	3408	1	303	QAGVHWRNLG\SLQPPPPPTLRRFS

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						CLSLPSSWDYRHPPSHPANFFFFFLL LVEARFHHVGQGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG
3149	8646	A	3409	3	1039	QQPFVNPALPPGYSTGLPYTGM SAFYQGPTMFVPPASAK*HGVNLT PTPPFQQPVGYGQHGYSTGYDDLT QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVSVSSSTTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCPTPTPTH LASPPAAPLTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCRLRQLSIL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFVNVIEVW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H
3150	8647	A	3410	2	344	LRQSVSLLPRTQAGVQWPNLGSLQ PPPPRFQRFSCLSLLSSWDYRHAPPC PTKF\VFLVET\GFTMLARLVIS*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSIL*SLQ\WPHV*SL AYSIL
3151	8648	A	3411	52	174	
3152	8649	A	3412	2	692	RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSFRRSPRGP ASPQR*PPRPDPWPPRQASPRCPT D*SRTFAGRTTDPQEEAVGGQGPSR GG*APSNSEPPLYGSGPLDSAFSLG TAFRKTLRIDLTQSQRPPHRSLSLYS GKGLAPGELADALNFLIYPTDFGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSPAKNFFSRY RHHS
3153	8650	A	3413	3	367	MLNYPLDFHPSFFVGGFFFMESRS\ VARLEVPVGVISSHCH\CLPGS\SDS PASASQVAGTT\GVCH*AQLIFVFLV ETGFHHFDQDGLDLTS*SVHLCPS KCWDYVIHPPQPPKVLGLQA
3154	8651	A	3414	1	595	MGIHHVGQASLELLTSGDLPASASQ GRGVRLYYNEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTSPYFWKPSLQTSPCSGSR SLWASLPSPLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL
3155	8652	A	3415	259	941	PVSWSLNSCRFFFFF*DQSLPSVV/Q AGSGQ*RNLDL\QPLASRFK*FSSS RL\SSW\DYRHMATMARLIFIFLVE MGF\TMLARLVNFLTSSDPPTSAFP KWLGLQGVPNTRAVGFN**LGYY SIILYHSNSPGTDLVFIYLFYTLFL RQEQNSAAQARVQ*WHNLGSLQSP PPGV\H*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR
3156	8653	A	3416	165	289	ISGLSGLYHIDRLIVCNCKQKPTYS